OM protein - protein search, using sw model

September 7, 2006, 11:54:20 ; Search time 40 Seconds Run on:

(without alignments) 536.408 Million cell updates/sec

Title: Perfect :

US-10-665-602-2 1249 1 MTWRHHVRLLFTVSLALQII......PSVLQRERRPCGRPGLGHRL 223 score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\* Database :

1: pirl: \* 2: pir2: \* 3: pir3: \* 4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Query Score Match Length DB ID	21.4 171 2 I	18.7 188	18.0 188	9.8 4391 2 A	121.5 9.7 1620 2 T27283 hypothetical prote	0.5 9.6 722 2 I48324 DELTA-like 1	.5 9.6 1372 2 T25933 hypothetical	119 9.5 810 2 T10756 Nel-homolog prot	118 9.4 2703 1 A24420 notch protei	116.5 9.3 2321 2 878549	115.5 9.2 2555 2 A40043	114.5 9.2 1574 2 T13954 MEGF6	114 9.1 1687 2 T30176 EGF re	113.5 9.1 1964 2 T09059 notc	113.5 9.1 2437 2 S42612 transme	112.5 9.0 1251 2 A57293 latent transfe	112.5 9.0 2524 2 A35844 Xotch protei	111 8.9 728 2 I50719 C-Delta-1	111 8.9 833 2 \$19087	111 8.9 861 2 A48825 Notch homo	111 8.9 1722 2 E89753 protei	111 8.9 2531 2 S18188	111 8.9 2531 2 A46019 notch-	111 8.9 3707 2 S18252 heparan	110 8.8 2318 2 S45306 notch 3 protein	109 8.7 2471 2 A49128 cell-fat	108 8.6 832 2 A31246 neurogenic		108 8.6 880 2 S00670
Score	267	233	225	123	121.5	120.5	120.5	119	118		115.5	114.5	114	113.5	113.5	112.5	112.5	111	111	111	111	111	111	111	110	109	108	108	•
Result No.	п	7	e	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	•

coagulation factor	Motch A protein -	protein apx-1 (imp	nel protein - chic	Wht inhibitory fac	fibropellin Ia - s	fibrillin 1 precur	hypothetical prote	hypothetical prote	glpl protein precu	t-plasminogen acti	Motch B protein -	fibrillin I - bovi	fibrillin-1 precur	zonadhesin - mouse	glycoprotein antig
KFHU12	B49175	D88991	JP0076	A59180	A40136	A47221	T22812	T15792	A32901	JS0597	A49175	A55567	A55624	T42215	865138
Н	~	N	~	~	~	~	N	~	~	~	~	~	~	~	7
'n	387	513	835	379	1064	3002	3871	907	1295	477	1203	2871	2871	5376	401
6	.,														
			8.3	8.2	8.2	8.2	8.2	8.2	8.2	8.1	8.1	8.1	8.1	8.1	8.1
	8.4	8.3	_	_	_	_					_	_	_	_	_

#### ALIGNMENTS

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teratocarcinoma-derived growth factor - mouse C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

A,Accession: 149612 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: mRNA A,Reaidues: 1-1/1 <RES>

A;Cross-references: UNIPROT:P51865; UNIPARC:UPI0000029326; GB:M87321; NID:g402714; PIDN: C;Genetics:

C;Superfamily: teratocarcinoma-derived growth factor 1; EGF homology A,Gene: cripto

63; Indels 18; Gaps Query Match 21.4%; Score 267; DB 2; Length 171; Best Local Similarity 37.8%; Pred. No. 9.7e-16; Matches 56; Conservative 11; Mismatches 63; Indels 1

ų,

58 FGEVTG-----SAEGWGPEEPLPYSRAF-----GEGASARPRCCRNGGTCVLGSFC 103 79 20 FGPVAGRDLAIRDNSIWDQKEPAVRDRSFQFVPSVGIQNSKSLNKTCCLNGGTCILGSFC g ठ

104 VCPAHFTGRYCEHDORRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCD----P 159 ð

80 ACPPSFYGRNCEHDVRKEHCGSILHGTWLPKKCSLCRCWHGQLHCLPQTFLPGCDGHVMD 139 g

SHILKASRIPCQIPSVITIFMLAGACLFL 167 160 KDFLASHAHGPSAGGAPSLLLLLPCALL 187 g ò

C. Species: Homo agaiens (man)
A. D. Hum. Genet. 49, 555-565, 1991
A. Title: Isolation and characterization of the CRIPTO autosomal gene and its X-linked re A. Reference number: A39787, MUID:9135371; PMID:1882841
A. Accession: B39787
A. Status: preliminary
A. Molecule type: DNA
A. Residues: 1-188 < DON>

A; Cross-references: UNIPROT: P13385; UNIPARC: UPI00004966D; GB: M96955; GB: M37099; NID: 933

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< DOM5 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;194-530/Domain: II <DOM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3687-4391/Domain: V
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F;4149-4151/Region:
F;4299-4301/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3845-3880/Domain:
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N.Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate prote porterate names: basement membrane heparan sulfate prote ().Alternate names: basement membrane membrane manes: basement membrane manes: basemence revision 07-Apr-1994 #text_change 12-Jul-2004 ().Bate: 07-Apr-1994 #sequence revision 07-Apr-1994 #text_change 12-Jul-2004 ().Accession: A38096; S19256; S7946; A41059; A40306; B33625; A38625; A41736 ().Biol. Chem. 267, B544-8557, 1992
A.Title: Primary structure of the human heparan sulfate proteoglycan from basement membr A.Title: Primary structure of the human heparan sulfate proteoglycan from basement membr A.Reference number: A38096; MUID:92235084; PMID:1569102
A.Accession: A38096 mNID:92235084; PMID:1569102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     teratocarcinoma-derived growth factor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: O-Mar-1992 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: A39387
R;Dono, R.; Montuori, N.; Rocchi, M.; De Ponti-Zilli, L.; Ciccodicola, A.; Persico, M.G. Am. J. Hum. Genet. 49, 555-565, 1991
Am. J. Hum. Genet. 49, 555-565, 1991
A.Title: Isolation and characterization of the CRIPTO autosomal gene and its X-linked re A;Reference number: A39787; MUID:9135371; PMID:1882841
R;Ciccodicola, A.; Dono, R.; Obici, S.; Simeone, A.; Zollo, M.; Persico, M.G.
EMBO J. 8, 1987-1991, 1989
A;Title: Molecular characterization of a gene of the 'EGF family' expressed in undiffere
A;Reference number: A30362; MUID:90005403; PMID:2792079
A;Accession: A30362
A;Molecule type: mRNA
A;Residues: 1-188 <CIC>
A;Cross-references: UNIPARC:UPI000004966D; GB:X14253; NID:g30220; PIDN:CAA32467.1; PID:g
C;Superfemily: teratocarcinoma-derived growth factor 1; EGF homology
C;Keywords: growth factor
F;78-106/Domain: EGF homology <EGF>
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A;Cross-references: UNIPROT:P98160; UNIPARC:UP10000168756; GB:M85289; NID:g184426; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 WPQEEP-----AIRPRSSQRVPPMGIQHSKELNRTCCLNGGTCMLGSFCACPPS 100
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A;Molecule type: DNA
A;Residues: 1-188 <DON>
A;Cross-references: UNIPROT:QSTCC1; UNIPARC:UPI0000145185
A;Note: the authors translated the codon GAC for residue 43 as Glu
C;Superfamily: texatocarcinoma-derived growth factor 1; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTGRYCEHDORRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCD 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTGRYCEHDORRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCD 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FYGRNCEHDVRKENCGSVPHDTWLPKKCSLCKCWHGOLRCFPQAFLPGCD 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.0%; Score 225; DB 2; Length 188; 38.2%; Pred. No. 4.1e-12; tive 7; Mismatches 31; Indels 30;
                                                                                                                                                                                                                                                                                                                                                                                           Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      30; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Score 233; DB 2;
Pred. No. 8.5e-13;
7; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WGPEEPLPYSRAFGEGASARPR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WGPEEPLPYSRAFGEGASARPR
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39.1%;
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Best Local Similarity 35...
A 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Kallunki, P.; Tryggvason, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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A;Residues: 1-810 «KUR»
A;Cross-references: UNIPROT:Q62919; UNIPARC:UP1000012FF2B; EMBL:U48246; NID:g3851179; PI<sup>I</sup>
A;Experimental source: strain Sprague-Dawley, brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P91526; UNIPARC:UPI0000075513; EMBL:U80815; PIDN:AAB37995.1; A;Experimental source: strain Bristol N2; clone W02C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kuroda, S.; Tokunaga, C.; Kiyohara, Y.; Konishi, H.; Matsuhashi, S.; Kikkawa, submitted to the EMBL Data Library, November 1998
A,Description: Protein kinase C-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                  91 CRNGGTC----VLGSFCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRACH-----LCRC 141
                                                                                                                                                                                                                                                                                                                                                                                              142 I--FGALHC---LPLQTPDRCDPKDFLASHAHGPSAGG------APSLLLLLPCA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nel-homolog protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                      451 CANGGICRDSVNDFSCICPPGYTGKNCSAPVSRCEHAPCHNGA----ICHQRGQRYMCEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 SARPRC----CRNGGTCVLGSF----CVCPAHFTGRYCEHDQRRSECGALEHGAWTLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1372;
                                                                                                                                                                  Length 722;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 4
A;Introns: 29/1; 66/1; 774/2; 823/2; 1046/1; 1108/2; 1298/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Murray, J.; Wohldmann, P. submitted to the EMBL Data Library, December 1996 A;Description: The sequence of C. elegans cosmid W02C12. A;Reference number: 220112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               349 AGGLOKC----ECSPGFTGERCETNIDECSTAHCPS 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 C-HLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPS 171
                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aypothetical protein W02C12.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.6%; Score 120.5; DB 2; ilarity 37.1%; Pred. No. 0.021; Conservative 7; Mismatches 35;
                                                                                                                                                                    DB 2;
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A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                               Score 120.5; DB Pred. No. 0.012; B; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 LLHRLLRPDAPAHPRSLVPSVLQRERRPCG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                564 AVVVCVŘLKLOKH------ÓPPPEPCG
                             homology
                       C;Superfamily: delta-4 protein; EGF hc
F;331-362/Domain: EGF homology «EGF2»
F;446-477/Domain: EGF homology «EGF2»
F;446-4515/Domain: EGF homology «EGF1»
                                                                                                                                                                  Query Match 9.6%;
Best Local Similarity 30.0%;
Matches 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-1372 <MUR>
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les 36; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T25933
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  A,Gene: Dll1
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 148324
R;Bettenhausen, B; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.
Development 121, 2407-2418, 1995
A;Title: Transient and restricted expression during mouse embryogenesis of D111, a murin
A;Reference number: 148324; MUID:95401858; PMID:7671806
F;65,71,76/Binding site: heparan sulfate (Ser) (covalent) #status predicted
F;89,554,1755,2121,3072,3105,3279,3780,3836,4068/Binding site: carbohydrate (Asn) (coval
F;2995,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UPI000017BCB4; EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: CESP:Y64G10A.£
A;Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1;
                                                                                                                                                                                                                                                                                                                                                                                              ----ALHC----HPEACGPDATCVNRPDGRGYTCRCHLGRSGLRCEEGVTVTTPSLSGAG 3936
                                                                                                                                                                                                                            85 SARPRCCRNGGTC----VLGSFCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRACHLCR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTCVLG-----SFCVCPAHFTGRYCEHDQRRSEC----GALEHGAWTLRACHLCRCIF 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 LNWISSHFGEVIGSAE-----GWGPEEPLPYSRAFGEGAS-----ARPRC----CRN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNFTSIFFREL-GEIEKLDFLPFNFHARKYLRFARFSRRGCSKCCLLRVQANCSADLCHN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5

127283

hypothetical protein Y64G10A.f - Caenorhabditis elegans

hypothetical protein Y64G10A.f - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T27283

R;Ainscough, R.

A;Reference number: Z20336

A;Reference number: Z20336

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1620 *MILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---ALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 GFELSGDGNTCSDIDECAVSNGGCSDRCVNSPGGFRCDCPSDLYLHADGRTCGKVTS
                                                                                                                                                                       58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
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                                                                                                               DB 2; Length 4391;
                                                                                                               Query Match 9.8%; Score 123; DB 2; Length 439
Best Local Similarity 27.3%; Pred. No. 0.037;
Matches 39; Conservative 4; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 121.5; DB 2; Length 1; Pred. No. 0.02; 14; Mismatches 63; Indels
                                                                                                                                                                                                                                                                              TCRDRPCQNGGQCHDSESSSYVCVCPAGFTGSRCEHSQ.
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-722 <RES>
                                                                                                                                                                                                                                                                                                                                         141 CIFGALHCLPLQTPDRCDPKDFLASHAHG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYLALPALTNTHHELRLDVEFKP 3959
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLLLLLPCALLHRLLRPDAPAHP 199
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nes 47; Conservative
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173 GGAPSLLLLLPCA 185
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Best Local Similarity
Matches 43; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: notch3
A;Map position: 19p13.1
C;Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        notch3 protein - human
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A; Residues: 1-2703 «KLD>
A; Residues: 1-2703 «KLD>
A; Cross-references: UNIPROT:P07207; UNIPARC:UPI000016BCC6; GB:K03508; NID:g157991; PIDN:
R; Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Teakonas, S.
Cell 43, 567-581, 1985
A; Reference number: A24768; MUID:86079539; PMID:3935325
A; Accession: A24768
A; Molecule type: mRNA
A; Residues: 1-48, 'I' 50-118, 'R', 120-230,'I', 232-256,'N', 258-266,'A', 268-872,'R', 874-958,
A; Residues: 1-48, 'I' 50-118,'R', 120-230,'I', 232-256,'N', 258-266,'A', 268-872,'R', 874-958,
A; Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
                                                                              4
                                                                                                                                          GEGASARPRC---CRNGGTCVLGSFCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRACH 137
                                                                                                                                                                                                              561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NyAlternate names: neurogenic repetitive locus protein
C;Species: Drosophila melanogaster
C;bacession: A24420; A24768; S09358; A05267
R;Kidd, S.; Kelley, M.R.; Young, M.W.
Mol. Cell. Biol. 6, 3094-3108, 1986
A;Reference number: A24420; MUID:87064624; PMID:3097517
A;Accession: A24420
                                                                                                                                                                                 510 GNGTICKAFCEEGCRYGGTCVAPNKCVCPSGFTGSHCEKDIDECAEGFVE-----CH
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A;Gene: notch; opa
A;Gross-references: FlyBase:FBgn0004647
A;Gross-references: FlyBase:FBgn0004647
A;Cross-references: B.96-9.36
A;Introns: 53/3; 84/3; 171/3; 240/3; 2833/3; 2436/3; 2588/3
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Keywords: differentiation; tandem repeat; transmembrane protein
F;27-328/Domain: EGF homology <EGRI>
F;280-561/Domain: EGF homology <EGFI>
F;568-599/Domain: EGF homology <EGFI>
F;988-1019/Domain: EGF homology <EGFI>
F;106-11218/Domain: EGF homology <EGRI>
F;106-11218/Domain: EGF homology <EGRIP
                                                                       14;
9.5%; Score 119; DB 2; Length 810; 39.2%; Pred. No. 0.018; Live 6; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    notch protein - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                              138 -LCRCIF--GALHC 148
                                                                                                                                                                                                                                                                                                                                                 562 NYSRCVNLPGWYHC 575
Query Match
Best Local Similarity 39.21
Matches 29; Conservative
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A,Accession: J. 2011.

A,Rolecule type: mRNA
A,Rolecule type: MID:g2668591; PII
A,Cross-references UNIPROT:Q9UM47; UNIPARC:UPI000011D827; EMBL:U97669; NID:g2668591; PII
R,Joutel, A., Corpechot, C.; Ducros, A.; Vahedi, K.; Chabriat, H.; Mouton, P.; Alamowitch
X, M.M.; Weissenbach, J.; Bach, J.F.; Bousser, M.G.; Tournier-Lasserve, E.
Nature 383, 707-710, 1996
A,Reference number: S71825; MUID:97032728; PMID:8878478
A,Reference number: S71825
A,Status: nucleic acid sequence not shown
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A;Residues: 67-113;138-194;268-333,'G',335-346;536-613;716-765;1240-1279;1815-1888 <JOUZ:
A;Cross-references: UNIPARC:UP10000177457; UNIPARC:UP10000177458; UNIPARC:UP1000177459;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 CQNGGTCVTQLNGKTYCACDSHYVGDYCEH---RNPCNSMRCQNGGTCQVTFRNGHPGIS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 CRNGGTCVL----GSFCVCPAHFTGRYCEHDORRSECGAL--EHGAW---TLRACH---L 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S78549; S71825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 GPEEPLPYSRAFGEGASARPRCCRNGGTCV--LGSF-CVCPAHFTGRYCEHDQRRSECGA
F;2538-2568/Region: glutamine-rich
F;2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>
                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2321;
                                                                                                                                                                                             1; Length 2703;
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32.3%; Pred. No. 0.075;
trive 5; Mismatches 50;
                                                                                                                                                                                      Query Match 9.4%; Score 118; DB 1;
Best Local Similarity 34.6%; Pred. No. 0.064;
Matches 28; Conservative 13; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Joutel, A.; Tournier-Lasserve, E. submitted to the EMBL Data Library, April 1997 A;Reference number: S78549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 CRCIFGALHCL-PLQTPDRCD 158
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A;Residues: 1-1687 <SEL>
A;Cross-references: UNIPROT:Q61204; UNIPARC:UPI00000280BB; EMBL:U57368; NID:g1336627; PI:
A;Experimental source: strain C57BL/6J; clone DBI-1; whole embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T09059
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Scismonted to the EWBL Data Library, October 1997
A;Description: _Sequence of the mouse major histocompatibility locus class III region.
A;Reference number: Z16543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Map position: 17
A; Map position: 17
A; Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67
A; Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67
C; Superfamily: notch protein; ankyrin repeat homology; EGF homology
C; Keywords: receptor; signal transduction
F; 514-545/Domain: EGF homology < EGF>
                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: T30176
NS 681, C.; Hoff III, H. B.
Submitted to the EMBL Data Library, May 1996
A;Description: Cloning of a novel mRNA regulated by the insulin like growth factor type
A;Reference number: 220762
A;Accession: T30176
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 CRNGGTC--VLGSF-CVCPAHFTGRYCEHDQRRSEC---GALEHGAWTLRACHLCRCIFG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 PLPYSRAFGEGASARPRCCRNGGTCVL---GSFCVCPAHFTGRYCEHDQRRSECGALEHG 129
605 GFYGKHCRKKCHCANRGRCHRL-YGACLCDPGLYGRFCHLA-CPPWAFGPGCSEDCLCEQ 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 INLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGEVTG-----SAEGWGPEE 72
                                                                                                                                                                                                                                                                                               EGF repeat transmembrane protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      904 IDTGSSYFCRCPPGFQGKLCQDNVNPCEPNPCHHGSTCVPQPSGYVCQCAPGYEGONCSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.1%; Score 113.5; DB 2; Length 1964; Best Local Similarity 24.1%; Pred. No. 0.12; Matches 67; Conservative 21; Mismatches 83; Indels 107; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 114; DB 2; Length 1687; Pred. No. 0.091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 CENGSTCTSVASQFSCKCPAGLTGQKCEAD--INECDIPGRCQHGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 ALHCLPLQTPDRCD-PKDFLASHAHGPSAGGAPSLLLLLPC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --rcinipgsyrcochogricohonspyvpcaps----pc 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1964 <ROW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.1%;
Best Local Similarity 34.7%;
Matches 35; Conservative
                                                                                                  : | |:|||
SHTRSCNPKD 672
                                                               153 TPDR-CDPKD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-1687 <S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 notch4 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: notch4
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                                                                                                                       A40043

notch protein homolog TAN-1 precursor - human

C;Species: Homo sapiens (man)

C;Accession: A40043

R;Ellisen, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, T.C.; Smith, S.D.; Sklar, Cell 66, 649-661, 1991

A;Title: TAN-1, the human homolog of the Drosophila Notch gene, is broken by chromosomal A;Reference number: A40043; MUID:91347367; PMID:1831692

A;Accession: A40043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Rebidues: 1-2555 <ELLA
A;Cross-references: UNIPARC:UPI0000177455; GB:M73980
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
F;261-292/Domain: EGF homology <EGET1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13954
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9693030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1574 <NAK>
A;Residues: 1-1574 <NAK>
A;Cross-references: UNIPROT: 088281; UNIPARC: UPI0000043BEE; EMBL: AB011532; NID: 93449293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 9.2%; Score 114.5; DB 2; Length 1574; Local Similarity 34.6%; Pred. No. 0.078; nes 45; Conservative 10; Mismatches 36; Indels 39; Gaps 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 GASARPRCCRNGGTCVL----GSFCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRAC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGWGP---EEPLPYSRAFGEGASARPRCCRNGGTC--VLGSFCVCPAHFTGRYCE---- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -------HDQRRSECGALEHGAWTL-----RACHLCRC---IFG---ALHCLPLQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGGTCISGPRSPTCLCLGPFTGPEC---QFPAS---SPCLGGNP 1396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCKGKP--CKNGGTCAVASNTARGFICKCPAGFEGATCENDAR--TCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 HLCRCIFG----ALHCLPLQTPDRCDPKDFLASHAHGPSAGGAP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Experimental source: strain Sprague-Dawley; brain C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F)98-1018/Domain: EGF homology <EGX2>
F)1149-1180/Domain: EGF homology <EGF>
F)1149-1264/Domain: EGF homology <EGF>
F)123-1264/Domain: EGF homology <EGR3>
F)1257-1959/Domain: ankyrin repeat homology <AN1>
F)196-1992/Domain: ankyrin repeat homology <AN1>
F)1994-2026/Domain: ankyrin repeat homology <AN2>
F)1994-2026/Domain: ankyrin repeat homology <AN3>
F)2027-2059/Domain: ankyrin repeat homology <AN3>
F)2027-Domain: ankyrin repeat homology <AN3>
F)2027-Domain: ankyrin repeat homology <AN3>
F)2027-2059/Domain: ankyrin repeat homology <AN3>
F)2060-2092/Domain: ankyrin repeat homology <AN5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 115.5; DB
Pred. No. 0.099;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.2%;
1266 GPGGGLTFTCHCA 1278
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Best Local Similarity
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RESULT 15
542612
Lransmembrane protein precursor - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: 342612
R;Bierkamp, C; Campos-Ortega, J.A.
R;Bierkamp, C; Campos-Ortega, J.A.
R;Bierkamp, C; Campos-Ortega, J.A.
R;Bierkamp, C; Campos-Ortega, J.A.
A;Title: A zebfrafish homologue of the Drosophila neurogenic gene Notch and its pattern C
A;Feferance number: 542612; MUD:94128602; FMID:8297791
A;Accession: 542612
A;Setue: pre-liminary
A;Molecule type: mRNA
A;Residues: 1-2437 <BIE>
A;Cusperfamily: notch protein; ankyrin repeat homology; EGF homology
F;755-786/Domain: EGF homology <EGF2>
F;1053-1054/Domain: EGF homology <EGF2>
F;1015-1947/Domain: ankyrin repeat homology <AN2>
F;1948-1980/Domain: ankyrin repeat homology <AN2>
F;1948-2014/Domain: ankyrin repeat homology <AN3>
F;2015-2014/Domain: ankyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
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                                                            1065 PGFTCHCPKGFEGPTCSHKALSCGIHHCHNGG----LCLPSPKPGSPPLCACLSGFGGP 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 PRC----CRNGGTCV--LGSF-CVCPAHFTGRYCEHDQRRSEC-----GALEHGAWT 132
                                                                                                                                                                           159 ------PKDP------LASHAHGPSAGGAPSLLLLLLP------CALLHRLLRP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Gaps
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9.1%; Score 113.5; DB 2; Length 2437;
Best Local Similarity 39.5%; Pred. No. 0.14;
Matches 32; Conservative 7; Mismatches 19; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                               1120 DCLTPPAPPGCGPPS-----PCLHNGTCTETPGLGN 1150
                                                                                                                                                                                                                                                                                                                                                           194 DA---PAHPRSLVPSVLQRERRPC-----GRPGLGH 221
130 AWTLRACH----LCRCIFGALH--CLPLQTPDRCD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: September 7, 2006, 11:59:50 Job time : 42 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

September 7, 2006, 11:51:00; Search time 297 Seconds (without alignments) 694.540 Million cell updates/sec Run on:

US-10-665-602-2 1249 1 MTWRHHVRLLFTVSLALQII......PSVLQRERRPCGRPGLGHRL 223 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2849598 seqs, 925015592 residues Searched:

2849598 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_7.2:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

SUMMARIES	Length DB ID Description	223 1 CFC1 HUMAN O9gzr3 homo sabien	1 CFC1 MOUSE P97766 mus m	193 1 CFC1 CHICK . 0918q3	2 Q504 <u>T</u> 5 BRARE Q504iS	183 2 057517_BRARE 057517	O57516_BRARE O57516	79 2 Q2VU94_XENLA Q2vu94 xeno	71 1 TDGF1 MOUSE P51865	2 Q3UZP8 MOUSE	2 Q7TQ06 MOUSE	2 Q2UZ96 XENLA	2 Q2UZ94 XENLA Q2uz94	2 Q2VU93_XENLA Q2vu93	CENLA Q2vu96	2 Q2UZ97_XENLA	2 Q800J2_XENLA Q800j2 xenopus	2 Q91649 XENLA	181 2 Q58D57_BOVIN Q58d57 bos t	188 1 TDGF1 HUMAN P13385 homo	2 Q8TCC1 HUMAN Q8tcc1 homo	1 TDGF2_HUMAN P51864 homo	66 2 Q9IATZ_BRARE Q9iat2 brack	763 2 Q4VB88_HUMAN Q4vb88	763 2 Q4VB91_HUMAN Q4vb91 homo	2061 2 Q4SRM9_TETNG Q4srm9	164 2 Q4RQ94_TETNG Q4rq9	714 1 DLL1 RAT	1 DLLA BRARE Q6di48	737 2 QGIRG3 XENLA	2 O52KG8_MOUSE Q52kg8	
	Query Match Length	99.4	39.1	25.8	22.9	22.8	22.1	21.5	21.4	21.2	21.2	21.1	20.9	20.9	20.9	20.0	19.9	19.9	19.4	18.7	18.7	18.0	14.3	10.8	∞.	ω.	9.	4.	10.4	10.4	10.2	
	Score	1241	488	322.5	286	285	275.5	269	267	265	265	263	261.5	261.5	261	249.5	248.5	248.5	242	233	233	225	178	135	135	134.5	132	130.5	130.5	130	127.5	
	Result No.	-	8	e	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23		25			28		30	

	Q9tvq2 caenorhabdi
06DJD9_XENLA 095RQ1_DROME 080GG9_CHICK 020245_CHICK 020YB41_HUWAN NELL1_HUWAN NELL1_HUWAN 06NSY8_HUWAN 05NSY8_HUWAN 05SBGG HUWAN 059BGB HUWAN 059BGB HUWAN 059BGB HUWAN	Q9TVQ2_CAEEL
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780 512 512 238 738 351 810 810 810 810 4391 4391 2331 2331	1651
011100100000000000000000000000000000000	9.7
127 125.5 125.5 123 123 123 123 123 123 123 123 123 123	121
00000000000000000000000000000000000000	45

### ALIGNMENTS

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99.4%;
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Matches 222; Conservative
                                     605376; phenotype.
608808; phenotype.
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52
97
103
114
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                                                                                             MEDLINE=228825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE=228825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Antschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Antschul K., Farmer A.H., Rubin G.M., Hong L., Stapleton M., Scares M.B., Foolald M.F., Casavant T.L., Scheez T.E., Stapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Antschaff B. M., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Antschaff S.J., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., McRand P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Nilalon D.K., Muzny D.W., Sodergen B.J., Lu X., Gibbs R.A., Febry J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Milting M., Madan A., Young A.C., Schwutz J., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., T. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PTM: N-glycosylated (By similarity).
-!- DISEASE: Defects in CFC1 are a cause of visceral heterotaxy (HTX2)
-!- DISEASE: Defects in CFC1 are a cause of visceral heterotaxy (HTX). HTX is characterized by a variable group of congenital anomalies that include complex cardiac malformations and situs inversus or situs ambiguus.
-!- DISEASE: Defects in CFC1 are a cause of transposition of the great arteries, dextro-looped (DTGA) [MIM:608008]. The more common form of DTGA, consists of complete inversion of the great vessels, so that the aorta incorrectly arises from the right ventricle and the pulmonary artery incorrectly arises from the left ventricle. This creates completely separate pulmonary and systemic circulatory systems, an arrangement that is incompatible with life. Patients of shunting that allow some mixing between the circulations in order to support life minimally, but surgical intervention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISEÁSE: Defects in CFC1 are a cause of conotruncal heart maiformations (CTHM) [MIM:217095]. CTHM consist of cardiac outflow tract defects, such a terralogy of Fallot, pulmonary arresia, double-outlet right ventricle, truncus arteriosus communis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muenke M.;
"CFG1 mutations in patients with transposition of the great arteries and double-outlet right ventricle.";
Am. J. Hum. Genet. 70:776-780 (2002).
An. J. Hum. Genet. 70:776-780 in the correct establishment of the left-right axis. May play a role in mesoderm and/or neural patterning during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goldmuntz E., Bamford R., Karkera J.D., dela Cruz J., Roessler E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT TRP-78, AND INVOLVEMENT IN DIGA AND CTHM.
PubMed=11799476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aortic arch anomalies.
SIMILARITY: Contains 1 EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF312769; AAG30294.1; -; mRNA.
EMBL; AF312925; AG42475.1; -; Genomic_DNA.
EMBL; BC063269; AAY14955.1; -; Genomic_DNA.
EMBL; BC069508; AAH69508.1; -; mRNA.
                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC074825; AAH74825.1;
BC074826; AAH74826.1;
BC110080; AAI10081.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, BC074825; AAH74825.
EMBL, BC010080, AAH74826.
BRBL, BC110080, AAI10081.
HSSP, P00750, 1TEC.
HGNC, HGNC.18292; CFCI.
MIM; 217095; phenotype.
Nature 434:724-731(2005)
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61 VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGREEVTKVATQKHRQSPLNWTSSHFGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shen M.M., Wang H., Leder P.;
"A differential display strategy identifies Cryptic, a novel EGF-
                                                                                                                                                                                                                                                                                                     . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                            EGF-like.

N.linked (GloNAc. ..) (Potential)
By similarity.
By similarity.
By similarity.
R - w (in dbSNP:2579433).
FTId=VAR 024322.
R - C (in HTX2; complete loss of activity; abnormal cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                 complete loss of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 223;
GO; GO:0007368; P:determination of left/right symmetry; NAS
                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24612 MW; B52852A00ABCF1A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CFC1_MOUSE STANDARD; PRT; 202 AA.
P97766; Q496U5; Q9J1B7; 20-DEC-2005, integrated into UniProtKB/Swiss-Prot.
01-MAY-1997, sequence version 1.
07-MAR-2006, entry version 30.
Cryptic protein precursor.
                                                                                                                                                                                                                                      Cryptic protein.
/FTId=PRO_000044630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1241; DB 1;
Pred. No. 7.7e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VAR 024324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTIG=VAR_024323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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DEVELOPMENTAL STAGE, AND GLYCOSYLATION.
STRAIN=129/Sv;
                    InterPro, IPR000742; EGF 3.
InterPro, IPR006209; EGF like.
InterPro, IPR013032; EGF like_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97178978; PubMed=9053319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muroidea; Muridae; Murinae; Mus
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related

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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        35
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65
105
111
122
83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
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                                                                               MUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klauaberg R.L., Zeeberg B., Bardow K.H., Schaefer C.F., Bhat N.K.,

A lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A platchenko L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

B stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i-TISSUE SPECIFICITY: No expressed in adult tissues.
-i-DEVELOPMENTAL STAGE: Expressed during gastrulation (from 6.5 dpc to 11 dpc) in two spatial domains that correspond to the axial and lateral mesoderm. In the first domain expression is progressively localized to the anterior primitive streak, the head process, and the node and notochordal. In the second domain, expression is initially concentrated in the lateral region of the egg cylinder, and is later found circumferentially in the intermediate and lateral plate mesoderm. Furthermore, the expression can also be detected at the early head-fold stage in the midline neuroectoderm, and consequently is an early marker for the prospective floor plate of the neural tube. Expression cases at the end of gastrulation, and has not been observed in later
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: Wice lacking functional Cfc1 showed positional defects in internal organs. The lung presents a right pulmonary isomerism. The stomerism is located on either the left or the right and the spleen is small and has an abnormal shape. The apex of the heart pointed to the right or left. In addition malpositioning of heart outflow tracts is observed, the acrta is connected to the right ventricle and emerged from the heart in a ventral position and to the right of the pulmonary artery. This one is connected to either the left or the right ventricle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLECTIDE SEQUENCE [GENOMIC DNA] OF 1-154.
MEDIINE-20480687; Pubmed=11024280; DOI=10.1016/S0378-1119(00)00337-1;
Colas J.-F., Schoenwolf G.C.;
"Subtractive hybridization identifies chick-cripto, a novel EGF-CFC ortholog expressed during gastrulation, neurulation and early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene expressed in the axial and lateral mesoderm during mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                Development 124:429-442(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 255:205-217(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION, AND KNOCK-OUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  embryonic stages.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiogenesis."
                          gastrulation.
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and

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65 AEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRRSECG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 ALEHGAWTLRACHLCRCIFGALHCLPLOTPDRCDPKDFLASHAHGPSAGGAPSLLLLLPC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 HHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGEVTGS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20480687; Pubmed=11024280; DOI=10.1016/S0378-1119(00)00337-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA], FUNCTION, AND DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gailus (Chicken).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00022; EGF 1; 1.
PROSITE; PS01186; EGF 2; FALSE_NEG.
PROSITE; PS50026; EGF 3; 1.
Developmental protein; EGF-like domain; Gastrulation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colas J.-F., Schoenwolf G.C.; "Subtractive hybridization identifies chick-cripto, a novel EGF-CFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.1%; Score 488; DB 1; Length 202; 54.6%; Pred. No. 2.4e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 P -> T (in Ref. 2; AAI00707)
21792 MW; 57035AD339A16FD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cryptic protein.

/FIGA-PRO_0000044631.

EGF-like.
N-linked (GlCNAc. ..)

By similarity.
By similarity.
By similarity.
P -> T (in Ref. 2; AAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Cripto-related factor 1)
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Q918Q3;
20-DEC-2005, integrated into UniProtKB/Swiss-Prot.
EMBL; U57720; AAC53042.1; -; mRNA.
EMBL; BC100705; AA100706.1; -; mRNA.
EMBL; BC100706; AA100706.1; -; mRNA.
EMBL; BC100706; AA100709.1; -; mRNA.
EMBL; BC100711; AA100712.1; -; mRNA.
EMBL; AF242430; AAF76323.1; -; Genomic_DNA.
HSSP; P00749; 1URK.
Ensembl; ENSMUSCO0000026124; Mus musculus.
MGI; MGI:109448; Cfc.1
GO, GO:0005615; C:extracellular space; TAS.
InterPro; IPR000742; EGF 3:
InterPro; IPR013032; EGF 3:
InterPro; IPR013032; EGF 1ike_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential
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173 GGAPSLLLLLPCALL 187
                                                                                                                                                                                                                                                        NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 L<sub>3</sub>191
                                                                                                        QS04IS BRARE
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                                                                                                                                                                                        Name=oep;
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                                                                                          BRARE
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Matches
                                                                              RESULT
Q50415
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                                                                                                                                          -I-FUNCTION: May play a role in mesoderm and/or neural patterning during gastrulation.

-I-FUNCTION: May play a role in mesoderm and/or neural patterning during gastrulation.

-I-DEVELOPMENTAL STAGE: First detected in the early-streak embryo, specifically in the epiblast layer. At the late streak stage, expression is condensed in the rostral half of the primitive streak. At HH stage 4 expression appeared for the first time in the mesendodermal layer of the presumptive prechordal plate rostrally and in the expanding mesoderm laterally. At HH stage 6, labeling in mesendodermal progenitors underlying the future forebrain level of the neuraxis reached its maximum, whereas mesoderm expression, which was restricted to the lateral plate, was accompanied by an underlying endodermal expression at the level of the heart-forming regions. Later gastrulation (HH stage level of the neural tube. Expressed in Hensen's node, within its mesenchymal core beneath the epiblast, and at a time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 SHFGEVTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 HDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCD---PKDFLASHAHGPSA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                               Schlange T., Schnipkoweit I., Andree B., Ebert A., Zile M.H., Arnold H.-H., Brand T., "Dual function of chicken cryptic in the determination of left-right asymmetry: control of midline barrier formation and lateralization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATOKHRQSPLNWTS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00008; EGF; 1. PR051TE; PS00022; EGF 1; 1. PR051TE; PS01186; EGF 2; PALSE NEG. PR051TE; PS0026; EGF 2; PALSE NEG. PR051TE; PS50026; EGF 3; PALSE NEG. Developmental protein; EGF-like domain; Gastrulation; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 25.8%; Score 322.5; DB 1; Length 193; l Similarity 34.9%; Pred. No. 5.9e-20; 68; Conservative 34; Mismatches 76; Indels 17
ortholog expressed during gastrulation, neurulation and early
                                                                                                                    the lateral plate mesoderm.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  r similarity.
E859A98F2DE6325F CRC64;
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/FTId=PRO_0000044632.
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AF228760; AAF97868.1; -; mRNA.
EMBL, AF228762; ARF97869.1; -; Genomic DNA.
EMBL, AF228761; AAF97869.1; JOINED; Genomic_DNA.
EMBL, AF282984; AAK07089.1; -; mRNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     when it is morphologically asymmetric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P00749; 1URK.
Ensembl; ENSGALG00000012623; Gallus gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000742; EGF_3.
InterPro; IPR006209; EGF_like.
InterPro; IPR013032; EGF_like_reg.
Pfam; PP00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115
38
N-
60
103
114
114
By
                                                     NUCLEOTIDE SEQUENCE [MRNA]
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              cardiogenesis.";
Gene 255:205-217(2000)
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DISULFID
SEQUENCE
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Best Local
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SIGNAL
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TISSUB-Embryo;

XX MISUINE-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Altachul S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Bhar N.K.,

Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Haidh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Appleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Gardan R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Gardan R.D., Mullahy S.J.,

X Richards S., Worley K.C., Hale S., Gardan R.D., Mullahy S.M.,

Yillalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield M., Schmin J.E., Jones S.J.M., Marra M.A.,

Butterfield M., Schmin J.E., Jones S.J.M., Marra M.A.,

Rodersation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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Ensembl; ENSDARG0000035095; Danio rerio.
ZFIN; ZDB-GENE-990415-198; oep.
InterPro; IPR013032; EGE_like_reg.
PROSITE; PS00022; BGF 1; UNKNOWN 1.
SEQUENCE 183 AA; 20374 MW; 5571447894E18507 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                         07-JUN-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                      183 AA
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                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                07-JUN-2005, sequence version 1.
07-FEB-2006, entry version 4.
Oep protein.
                                                                                                                                                                                                                                      PRELIMINARY;
172 QQTMSALICLLTFLL 186
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183

BRARE

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71 EEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRRSECGALEHGA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                               65 EAALPFVGLTGVAKQSR-TCCKNGGTCILGSFCACPKYFTGRSCEYDERLRDCGVIPHGE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 WTLRACHLCRCIFGALHCLP-----LQTPDRCDPKDFLASHAHGPSAGGAPSLLLLL 182
                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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PubMed=16339189; DOI=10.1242/dev.02188;
Onuma Y., Yeo C.Y., Whitman M.;
"XCR2, one of three Xenopus EGF-CFC genes, has a distinct role in the regulation of left-right patterning.";
Development 133:237-250(2006).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GEVTKVATOKHROSPLN
                                                                                                                                                                                                                                                                                                                                                                       11; Gaps
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOTEY K., Hill C.S.; Release in Nodal signalling during early
permissive EGF-related ligand required during gastrulation."; Cell 92:241-251(1998).
                                                                                                                                                                                                                                                                                                                          Length 190;
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Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                     EMBL; AF041440; AAC04338.1; -; mRNA.
HSSP; P00750; 1TPG.
ERSembl; WRNDARGO0000035095; Danio rerio.
ZFIN; ZDB-GENE-990415-198; oep.
IILCETPO; IPRO13032; EGF like reg.
PROSITE; PS0022; EGF like reg.
SEQUENCE 190 AA; 21199 WW; 8D127CAD0625D28A CRC64;
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EMBL, AJ864900; CA115754.1; -; mRNA.
EGF-like domain; Repeat.
SEGUENCE 179 AA; 20060 WW; 912E723BE597D6CE CRC64;
                                                                                                                                                                                                                                                                                                                     Query Match 22.1%; Score 275.5; DB 2; Best Local Similarity 41.1%; Pred. No. 7.2e-16; Matches 53; Conservative 18; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MTWRHHVRLLFTVSLALQ-IINLGNSYQREXHNGGR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JAN-2006, integrated into UniProtKB/TrEMBL.
10-JAN-2006, sequence version 1.
07-MAR-2006, entry version 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Q2VU94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|||||
182 ATFILHRLL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 PCALLHRLL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
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Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
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           셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 WTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLLLLPCALLHRL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 WVQKGCSYCRCGYGLLHCFPHVFSKDCDDSQEVRWHRSG-SLRTLSSTIVMFATFILHRL
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
MEDLINE=9817252; PubMed=9458048; DOI=10.1016/S0092-8674(00)80918-6;
Zhang J., Talbot W.S., Schier A.F., F.
"Positional cloning identifies zebrafish one-eyed pinhead as a
permissive EGF-related ligand required during gastrulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98117252; PubMed=9458048; DOI=10.1016/S0092-8674(00)80918-6; Zhang J., Talbot W.S., Schier A.F.; "Positional cloning identifies zebrafish one-eyed pinhead as a
                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii; Teleostei; Ostariophysi, Cypriniformes,
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.8%; Score 285; DB 2; Length 183; 43.0%; Pred. No. 1e-16; tive 16; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20405 MW; 1471447894E1851B CRC64;
                                                                                                                                                                                     01-JUN-1998, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ensembl; ENDDARGG000035095; Danio rerio.
ZFIN; ZDB-GENE-990415-198; oep.
ThterPro; IPR013032; EGF like reg.
PROSTIE: 100022; EGF 1; UNKNOWN 1.
SEQUENCE 183 AA; 20405 WW; 14714478941
                                                                                                                                                                                                        01-JUN-1998, sequence version 1.
07-FEB-2006, entry version 24.
One-eyed pinhead short form protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF041441; AAC04339.1; -; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 sequence version 1.
07-FEB-2006, entry version 23.
One-eyed pinhead long form protein.
                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell 92:241-251(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P00750; 1TPG
                                                                                                                                                                                                                                                                                                                                                                       Cyprinidae, Danie
NCBI_TaxID=7955;
                            Ĺ 183
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057517;
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InterPro; IPR013032; EGF_like_reg.
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CARBOHYD
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                                                      49 --VDHAGKEKSSV-----ETIPFI-GLTKNHALDKHCCKNGGTCVLGSFCACPKHYTGR 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of the mouse Tdgf1 gene and Tdgf pseudogenes.";
Mamm. Genome 7:344-348(1996).
-!- FUNCTION: Could play a role in the determination of the epiblastic
                               53 WTSSHFGEVTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGR
                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
    1 MVW---LKRLFYLTVQLSAVIRLGT----PKQNGTMINAGSELSEDTYVQKLLHH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129/Sv;
MEDLINE=5625959; PubMed=8661720; DOI=10.1007/8003359900100;
Liguori G., Tucci M., Montuori N., Dono R., Lago C.T., Pacifico A.F.,
Persico M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells that subsequently give rise to the mesoderm.

TISSUE SPECIFICITY: Expressed at low level in specific organs of
the adult animal such as spleen, heart, lung and brain. During
gastrulation, expressed in the forming mesoderm. In later stages
of the developing heart, expression is restricted to the truncus
                                                                                                                                                                                                         01-0CT-1996, integrated into UniProtKB/Swiss-Prot.
01-0CT-1996, sequence version 1.
07-MAR-2006, entry version 40.
Teratocarcinoma-derived growth factor precursor (Epidermal growth factor-like Cripto protein) (Cripto growth factor).
Name-Tdgf1; Synonyms-Cripto;
                                                                                                                                                                                                                                                                                                                                                                                                                                             "The murine cripto gene: expression during mesoderm induction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STACE: First expressed prior to the onset of gastrulation (early streak stage), then continues throughout
                                                                                    113 YCEHDORRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFL 163
                                                                                               100 YCELHVHNRKCGIVPHGHWVQKKCALCRCMYGTMHCFP---SGDCDAKDYV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ensembl, ENSWINSGOUGO032494; Mus musculus.
Ensembl, ENSWINSGOUGO032494; Mus musculus.
MG1:98658; Tdgf1.
GG; GG:0003615; C:extracellular space; TAS.
GG; GG:0010763; P:branching morphogenesis; IDA.
GG; GG:0001763; P:branching morphogenesis; IDA.
GG; GG:0001763; P:branching morphogenesis; IDA.
GG; GG:00005595; P:determination of anterior/posterior axis, e...
GG; GG:0007507; P:heart development; IDA.
GG; GG:0000595; P:posttive regulation of cell migration; IDA.
InterPro; IPR006209; EGF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                    , Scalera L., Pacifico F., Acampora D., Persico M.G.,
                                                                                                                                                                                 171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          embryonic development.
-!- SIMILARITY: Contains 1 EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M87321; AAA37459.1; -; mRNA.
EMBL; X94083; CAA63827.1; -; Genomic_DNA.
PIR; 149612; 149612.
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6; TISSUE=Embryo;
MEDLINE=94094736; PubMed=7916676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Development 118:1157-1168(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE OF 135-171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               early heart morphogenesis."
                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arteriosus.
                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                   Simeone A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; 149
HSSP; P0
Ensembl;
MGI; MGI
                                                                                                                                                                                             P51865;
                                                                                                                                                                    MOUSE
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104 VCPAHFTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCD----P 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CSTBL/6J; TISSUE-Whole body;
PubMed=16141072; DOI=10.1126/science.1112014;
PubMed=16141072; DOI=10.1126/science.1112014;
PubMed=16141072; DOI=10.1126/science.1112014;
Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Parest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla B.P., Dalrymple B.P., de Bono B., Della Gatte G., Crowe M.L., Dalla B.P., Fukushina T., Fugetcher C.F., Fukushina T., Furuno M., Futaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 FGPVAGRDLAIRDNSIWDQKEPAVRDRSFQFVPSVGIQNSKSLNKTCCLNGGTCILGSFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGEVTG-----SAEGWGPEEPLPYSRAF-----GEGASARPRCCRNGGTCVLGSFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CS7BL/63; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-0CT-2005, integrated into UniProtKB/TrEMBL.
11-0CT-2005, sequence version 1.
21-FEB-2006, entry version 8.
6 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5630400Fl3 product:teratocarcinoma-derived growth factor, full
                                                                                                                                                   Teratocarcinoma-derived growth factor
                                                                                                                                                                                                                                  . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   C52051AEACDB5380 CRC64;
                                                                                                  Growth factor; Signal
                                                                                                                                                                              /FTId=PRO_0000007504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.4%; Score 267; DB 1; 37.8%; Pred. No. 3.5e-15;
                                                                                                                                                                                                                               N-linked (GlcNAc.
                                                                                                                                                                                                                                                       By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 KDFLASHAHGPSAGGAPSLLLLLPCALL 187
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InterPro; 1rnv1.
                                                                                                                                                                                                      91 EG
63 N-
73 By
79 By
90 By
117 By
124 WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 MOUSE
QJUZP9 MOUSE PRELIMINARY;
QJUZP9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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Name=Tdgf1;
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ARAINESTED SEQUES Whole body;

RYGLEGITLE SEQUES SEQUES WHOLE body;

RYGLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA OKAZAKI Y., FURTUN M., KASUKAWA T., Adachi J., Bono H., Kondoo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yegi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Blake J.A., Bradt D., Buusic V., Chothia C., Corbani L.E., Cousins S.,

Balke J.A., Bradt D., Russic V., Chothia C., Corbani L.E., Cousins S.,

Rasterland T., Gariboldi M., Gissi C., Godzik A., Frazer K.S.,

Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Ronagaya A., Kurochkin I.V., Lee Y., Lehkard B., Lyons P.A.,

Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ringwald M.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ringwald M.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Sultana R., Takenaka Y., Zimmer A., Satou M., Shimada K.,

Werardo R., Wanner L., Wahlestedt C., Wang Y., Watanabe Y., Walls C.,

Willming L.G., Wynshaw-Boris A., Yanagiawa M., Sakaume N., Sakavatue N., Sato K.,

Rayaski T., Wanki K., Kawai J., Alzawa K., Sakavatue N., Stukuda S.,

Rayazaki T., Waki K., Ishingawa T., Fukuda S.,

Rayazaki T., Waki K., Ishingawa T., Itoh M., Kagawa I.,

Mayazaki A., Sakaki N., Sasaki D., Shibata K., Shibagawa A.,

Mayazaki A., Sakaki K., Sasaki D., Shibata K., Shibagawa A.,

Mayazaki A., Sakaki K., Sasaki D., Shibata K., Shibagawa A.,

Mayazaki A., Sakaki K., Sasaki D., Shibata K., Shorer J. Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
Jak M., Kanapin A., Katoch M., Kawasawa Y., Kalson J., Kitamura H.,
Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
Mottaguli-Tabar S., Mider N., Nakauchi H., Ng P.,
Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
Nokazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schostder C.,
Schoubach C., Setiguchi K., Semje C.A., Seno S., Sessa L., Sheng Y.,
Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
Juda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
Vamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Otackenbush J.,
Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasski D., Tomaru Y.,
Rukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
Ilda J., Imamura K., Itch M., Kato T., Kawaji H., Kawagahira N.,
Kawashima T., Kojima M., Kondo S., Konno H., Nikain T., Suzuki S.,
Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki J., .., Hayashizaki Y.: s of the mouse transcriptome based on functional annotation of s of the mouse transcriptome STRAIN=C57BL/6J; TISSUB=Whole body;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566(2005). Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005). full-length cDNAs."; NUCLEOTIDE SEOUENCE NUCLEOTIDE SEQUENCE Hayashizaki Y.; Birney E "Analysi 

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Rachina M., Gassterland T., Gissi C., King B., Kochiwa H., Rachel P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Ra Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Iyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N., A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P., Whishaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Marshiya Y., Kawaji H., Kohtsuki S., GO; GO:0005615; C:extracellular space; RCA. GO; GO:0019897; C:extrinsic to plasma membrane; IDA. GO; GO:0008595; P:determination of anterior/posterior axis, e. . .; IMP. Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License STRAIN=C57BL/6J; TISSUE=Whole body; MEDLINE=20499374; PubMed=11042159; DDI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nutamatsu M., Hayashizaki Y.; Pubmatizaki Y.; Pubmatsu M., Hayashizaki Y.; Shibata to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000). Gaps MUCLIOLIDE SUCCESTER, CALL TISSUE=Whole body;
Shibatra = C57BL/6J; PubMed=11076861; DOI=10.1101/gr.152600;
Shibatca K., Nacaoka K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Natunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamannoto R., Matsumoto H., Sakaguchi S., Ikagami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Narakatru M., Inoue Y., Kira A., Hayashizaki Y.; Rikiki integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000). ATRAIN=CSTREL/6J; TISSUE=Whole body;
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Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.,
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; 18; Length 171; Indels C53400FDEEBF6380 CRC64; 21.2%; Score 265; DB 2; L 37.8%; Pred. No. 5.3e-15; iive 11; Mismatches 63; EMBL; AK133730; BAE21807.1; -; mRNA. InterPro; IPRO13032; EGF like reg.
PROSITE; PS00022; EGF 1; UNKNÖWN 1.
PROSITE; PS50026; EGF 1; UNKNÖWN 1.
CEC11 adhesion; EGF 3; 1.
SEQUENCE 171 AA; 18646 MW; C534( Conservative Nature 409:685-690(2001). InterPro; IPR000742; EGF\_ InterPro; IPR013032; EGF\_ MGI:98658; Tdgf1. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE Best Local Similarity 26; Query Match Matches 

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STRAIN-C57BL/6J; TISSUE-Whole body; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

Nature 420:563-573(2002). NUCLEOTIDE SEQUENCE α

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Xenopodinae; Xenopus; Xenopus
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FGEVTG-----SAEGWGPEEPLPYSRAF-----GEGASARPRCCRNGGTCVLGSFC 103
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MGI: MGI: 98658; Td9fi.

GO; GO:0008515; C:extracellular space; RCA.

GO; GO:001897; C:extrinsic to plasma membrane; IDA.

GO; GO:0008595; P:determination of anterior/posterior axis, e. .; IMP.

InterPro; IPR006742; EGF 3.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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PROSITE; PS50026; EGF 3; 1.
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"Role of EGF-CFC family members in Nodal signalling during early
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SEQUENCE 191 AA; 21651 MW; D4E992122C89495D CRC64;
adhesion; EGF-like domain.
ENCE 171 AA; 18655 MW; C53400EBACDB5380 CRC64;
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21.2%; Score 265; DB 2;
Best Local Similarity 37.8%; Pred. No. 5.3e-15;
Matches 56; Conservative 11; Mismatches 63.
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"Role of EGF-CFC family members in Nodal signalling during early
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                                                                                                                                                                                                                                                 DB 2; Length 251;
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                                                                                                                                                                                                                                                                                  21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Indels
                                                                                  Xenopus development.";
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                 omain; Repeat.
251 AA; 27813 MW; D0256376A829A37E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGF-like domain; Repeat.
SEQUENCE 251 AA; 27849 MW; DODFCC140A3EOBFE CRC64;
                                                                                                                                                                                                                                                20.9%; Score 261.5; DB 2; 54.1%; Pred. No. 1.6e-14; iive 10; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JAN-2006, integrated into UniProtKB/TrEMBL.
10-JAN-2006, sequence version 1.
07-MAR-2006, entry version 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Embryo stage 10.5;
PubMed=16339189; DOI=10.1242/dev.02188;
Onuma Y., Yeo C.Y., Whitman M.;
"XCR2, one of three Xenopus EGF-CFC genes,
regulation of left-right patterning.";
Development 133:237-250(2006).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Mismatches
                                                                                                                                                                                  EMBL; AJ864901; CAI15755.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenobus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AY796189; AAX81599.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QZVU93_XENLA PRELIMINARY;
                                                                                                                                                                                                                                                               1 Similarity 54.1%;
40; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CR3 long transcript variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | || || ::
P---SGDCDAKDYV 219
                                                                                                                                                                                                                                                                                                                                                                                                       150 PLQTPDRCDPKDFL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 PLQTPDRCDPKDFL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                 EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8355;
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                    90
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                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                   Query Match
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RESULT CONTROL OF CONT

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52 NWTSSHFGEVTGSAEGWGP---EEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 NTISQFLQDTINATHGKSPVKSAKTLPF-LGITDSKKLNRKCCQNGGTCFLGTFCICPKQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 CCRNGGTCVLGSFCVCPAHFTGRYCEHDQRRSECGA-LEHGAWTLRACHLCRCIFGALHC 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                         PubMed=16339189; DOI=10.1242/dev.02188; Onuma Y., Yeo C.Y., Whitman M.; Onuma Y., one of three Xenopus EGF-CFC genes, has a distinct role in the regulation of left-right petterning."; Development 133:237-250(2006).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 CCNNGGTCVLGSFCVCPRYFTGRHCEYDERAKHCTAKIQHGDWIRKGCRLCRCAYGVLHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Gaps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Annura; Mesobatrachia; Pipoldea; Pipidae; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dorey K., Hill C.S.; "Role of EGF-CFC family members in Nodal signalling during early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Match 20.9%; Score 261; DB 2; Length 191; Local Similarity 52.4%; Pred. No. 1.3e-14; les 43; Conservative 12; Mismatches 25; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY796186; AAX81596.1; -; mRNA.
SEQUENCE 191 AA; 21681 MW; 95E9920E40F95531 CRC64;
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SEQUENCE 190 AA; 21455 WW; F7C5E388CDBB05BA CRC64;
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Search completed: September 7, 2006, 11:59:05 Job time: 299 secs

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Query Match 100.0%; Score 1249; DB 4; Best Local Similarity 100.0%; Pred. No. 1.2e-103; Matches 223; Conservative 0; Mismatches 0;
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-665-602-2
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Sequence 98, Appl
Sequence 101, App
Sequence 198, App
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231675,
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Sequence 1293, A
Sequence 2712, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                                                                                                                                                                           (without alignments)
593.660 Million cell updates/sec
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1 MTWRHHURLLFTUSLALQII.......PSVLQRERRPCGRPGLGHRL 223
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                                                                                                                                               September 7, 2006, 12:11:27; Search time 174 Seconds
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-764-893-98
US-09-764-893-98
US-09-764-891-101
US-09-764-891-101
US-10-073-865-98
US-10-073-865-98
US-10-295-027-1293
US-10-295-027-1293
US-10-295-027-1293
US-10-295-027-1293
US-10-2940-431-4
US-10-940-431-6
US-10-940-431-1
US-10-390-566-7
US-10-390-566-7
US-10-390-566-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/065,602
FILING DATE: 22-Sep-2003
CLASSIFTCATION COMPATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/393,023A
FILING DATE: 06-JUN-1999
APPLICATION NUMBER: US/09/393,023A
TTORNEY/AGRY INFORMATION:
NAME: Marks, Michelle S.
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PF200D1
TELEPHONE: 301-309-8504
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| Publication No. US20040086967A1
| GENERAL INFORMATION:
| APPLICANT: Meissner, Paul S.
| TITLE OF INVENTION: Human Criptin Growth Factor NUMBER OF SEQUENCES: 7
| CORRESPONDENCE ADDRESS: 7
| ADDRESSEE: Human Genome Sciences, Inc. |
| STREET: 9410 Key West Avenue CITY: Rockville
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US-10-712-124-58
US-10-693-538-1
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US-10-491-997-28
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COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
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Length 223;

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Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 192 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 101'
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Patent No. US20020090672A1
GENERAL INFORMATION:
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Matches 223; Conservative
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
CURRENT FILING DATE:
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LENGTH: 229
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-893-98
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MTWRHHVRLLFTVSLALQI INLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PUZO9
CURRENT APPLICATION NUMBER: US/09/764,893
CURRENT FILING DATE: 2001-01-19
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 154
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 98
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US-09-764-881-101
Sequence 101, Application US/09764881
Publication No. US20020086821A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION Nucleic Acids, Proteins, and Antibodies;
FILE REFERENCE: PT207
CURRENT APPLICATION NUMBER: US/09/764,881
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ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
ORGANISM: SITE
LOCATION: (2)
OCTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-608
                                                                                                                                                                                   LOCATION: (3)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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APPLICANT: ROSEEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PUZ06
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
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100.0%; Pred. No. 1.2e-103;
iive 0; Mismatches 0;
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100.0%; Score 1249; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.2e-103;
Matches 223; Conservative 0; Mismatches 0;
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   LENGTH: 229
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LOCATION: (2)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT207
CURRENT APPLICATION NUMBER: US/09/764,881
CURRENT APPLICATION NUMBER: US/09/764,881
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 192
SOFFWARE: Patentin Ver. 2.0
SEQ ID NO 101
                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE REFERENCE: PZ01
FILE REFERENCE: PZ020
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 311
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 269
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Patent No. US20020090673A1
GENERAL INFORMATION:
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Publication No. US20030125246A9
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-764-881-101
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TYPE: PRT
ORGANISM: Homo sapiens
ORGANISM: STE
NAME/KEY: SITE
LOCATION: (2)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-881-101
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LOCATION: (2)
LOCATION: (2)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
NAME/KEY: (1)
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Publication No. US20030044904A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P0Z9GC1
CURRENT APPLICATION UNMBER: US/10/073,865
CURRENT FILING DATE: 2002-02-14
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NUMBER OF SEQ ID NOS: 154
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 98
LENGTH: 229
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                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 1249; DB 3; Best Local Similarity 100.0%; Pred. No. 1.2e-103; Matches 223; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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NUMBER OF SEQ ID NOS: 192
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JETCANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: Pr207C1

CURRENT APPLICATION NUMBER: US/10/242,747

CURRENT FILING DATE: 2002-09-13

PRIOR APPLICATION NUMBER: 09/764,881

PRIOR APPLICATION NUMBER: 00/179,065

PRIOR APPLICATION NUMBER: 60/180,628

PRIOR APPLICATION NUMBER: 60/180,628

PRIOR PILING DATE: 2000-00-01-31

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2000-00-14

PRIOR PILING DATE: 2000-00-07-11

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2000-08-14

PRIOR PILING DATE: 2000-08-14

PRIOR PILING DATE: 2000-07-16

PRIOR PILING DATE: 2000-07-16

PRIOR PILING DATE: 2000-07-14

PRIOR PILING DATE: 2000-07-14
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                                                                                                                                                                                                                                         US-10-242-747-101
Sequence 101, Application US/10242747; Publication No. US20040005577A1
GENERAL INFORMATION:
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NAME/KEY: SITE
1 LOCATION: (44)
2 COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-198
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APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
ITILE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
      Sequence 198, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Mucleic Acids, Proteins, and Antibodies
; FILE REPRENCE: PJZ01
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 198
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Best Local Similarity 99.6%; Pred. No. 5.2e-103;
Matches 222; Conservative 0; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2001-11-13
PRIOR PLICATION NUMBER: US 60/335,394
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR APPLICATION NUMBER: US 60/335,464
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Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Richard
APPLICANT: Glynne, Richard
APPLICANT: Hevezl, Perer A.
APPLICANT: Havezl, Perer A.
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ORGANISM: Homo sapiens
US-09-764-898-198
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APPLICATION NUMBER: US 60/340,376
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CURRENT APPLICATION NUMBER: US 09/663,733
PRIOR PILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR PILING DATE: 2001-11-15
PRIOR PILING DATE: 2001-11-15
PRIOR PILING DATE: 2001-11-21
PRIOR PILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
          PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-14
PRIOR PILING DATE: 2001-12-14
PRIOR PPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/355,714
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR APPLICATION ALWER: 2002-02-13
PRIOR PILING DATE: 2002-02-13
PRIOR PILING DATE: 2002-02-13
PRIOR PLING DATE: 2002-02-13
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Publication No. US20030232350A1
GENERAL INFORMATION:
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APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsh, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
2001-11-21
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Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-422
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Sequence 2712, Application US/10264237

Sequence 2712, Application US/10264237

Publication No. US20040009491A1

GENERAL INFORMATION:

TITLE OF INVENTION: No.elect Acids, Proteins, and Antibodies

FILE REFERENCE: PA131P1

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR APPLICATION NUMBER: DCT/US01/16450

PRIOR APPLICATION NUMBER: DCT/US01/16450

PRIOR PILING DATE: 2000-05-19

NUMBER OF SED ID NOS: 2876

SOFTWARE: PatentIN Ver. 3.1

SEQ ID NO 2712

LENGHI 223

TVDE: DER
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Pred. No. 6.1e-103;
0; Mismatches 1; Indels (
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PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR PILING DATE: 2002-01-09
PRIOR PILING DATE: 2002-01-09
PRIOR PILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-13
PRIOR FILING DATE: 2002-02-13
PRIOR FILING DATE: 2002-02-13
SOFTWARE: PATENT NOW 1386
SOFTWARE: PATENT NOS: 1386
SOFTWARE: PATENT NOS: 1386
LENGTH: 223
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Best Local Similarity 99.6%;
Matches 222; Conservative
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US-10-295-027-1293
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CRGANISM: Homo sapiens
US-10-264-237-2712
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Length 223;

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125 ALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLLLLLPC 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10940431
; Sequence 3, Application US/10940431
; Publication No. US20050208045A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie
; APPLICANT: Harrison, Craig A.
; TITLE OF INVENTION: Signaling
; TITLE OF INVENTION: Signaling
; FILE REPERBNCE: D6525
; CURRENT APPLICATION NUMBER: US/10/940,431
; CURRENT APPLICATION NUMBER: US/10/940,431
; CURRENT FILING DATE: 2004-09-14
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Macintosh OS 10
; SEQ ID NO 3
; LENTER TO THE TOWN OF 
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39.1%; Score 488; DB 5; Length 20
Best Local Similarity 54.6%; Pred. No. 1.6e-35;
Matches 100; Conservative 16; Mismatches 65; Indels
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                                                                                        98.7%; Score 1233; DB 4;
99.1%; Pred. No. 3.2e-102;
tive 0; Mismatches 2;
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Matches 221; Conservative
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ORGANISM: Mus musculus
ORGANISM: Homo sapiens
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   ; ORGANISH: ...
US-10-257-113-2
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                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10940431
; bublication No. US200S0208045A1
; bublication No. US200S0208045A1
; GENERAL INFORMATION:
; APPLICANT: Wale, Wylie
; APPLICANT: Harrison, Craig A.
; TITLE OF INVENTION: Grapto Antagonism of Activin and TGF-(
; TITLE OF INVENTION: Signaling
; FILE REFERENCE: D6525
; CURRENT APPLICATION NUMBER: US/10/940,431
; CURRENT FILING DATE: 2004-09-14
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Macintosh OS 10
; SEQ ID NO 4
; SEQ ID NO 4
; SEQ ID NO 4
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; Sequence 2. Application US/10257113
; Publication No. US20030207293A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: CRYPTIC-LIKE SECRETED PROTEIN
; FILE REFERENCE: MERCK-2519
; CURRENT APPLICATION NUMBER: US/10/257,113
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: EP 00107142.2
; PRIOR PILING DATE: 2000-04-10
; NUMBER OF SEQ 1D NOS: 2
; SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 223
; TYPE: PRT
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US-10-257-113-2
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1: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US08_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US08_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US00_NEW_PUB.pep:*
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1 MTWRHHVRLLFTVSLALQII......PSVLQRERRPCGRPGLGHRL
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US-10-669-920-22

US-10-505-928-150

US-11-217-997-36

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US-11-071-796A-22

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US-11-75-714-8

US-11-75-714-11
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Maximum Match 100%
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No.
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ý,	Sequence 5, Appli	Sequence 22, Appl	Sequence 21, Appl	Sequence 38, Appl	Sequence 30, Appl	Sequence 27, Appl	Sequence 12, Appl	Sequence 2, Appli	Sequence 22, Appl	Sequence 16, Appl	Sequence 20, Appl	Sequence 18, Appl	Sequence 42, Appl	Seguence 40, Appl	Sequence 3263, Ap	Sequence 37, Appl	Sequence 8, Appli	Sequence 7, Appli	Sequence 12, Appl
~	US-11-054-369A-5	US-11-178-724-22	US-11-071-796A-21	US-11-217-997-38	US-11-217-997-30	US-11-178-724-27	US-11-217-997-12	US-11-217-997-2	US-11-217-997-22	US-11-217-997-16	US-11-217-997-20	US-11-217-997-18	US-11-217-997-42	US-11-217-997-40	US-11-293-697-3263	US-10-781-841-37	US-11-264-243-8	US-11-175-714-7	US-11-288-992-12
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8.8	8.8	8.8	8.8	8.7	8.6	9.8	9.8	9.8	9.8	8.6	8.6	9.6	8.6	9.8	8.6	9.8	9.8	8.5	8.4
110.5	109.5	109.5	109.5	109	108	108	108	108	108	108	108	108	108	108	107	107	107	106	104.5
56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

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RESULT 1

15. Sequence 5. Application US/1117514

15. Sequence 5. Application US/1117514

15. Sequence 5. Application US/1117514

15. Publication No. US20060122373A1

15. Sequence 5. Application No. US20060122373A1

15. Sequence 5. Application No. US2006012373A1

15. Septicant McCartby, Sean A. Applicant McCartby, Charles Applicant McCartby, Charles Applicant McCartby, Charles Applicant McCartby, McCartby, Charles Applicant McCartby, Septicant McCartby, McCartby, Charles Applicant McCartby, Septicant McCartby, McCartby
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Publication No. US20060104898A1
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APPLICANT: WATANABE, TAUTOMU
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: HORIE, MASATO
TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
FILE REFERENCE: Q-5359
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: US/10/342,276
PRIOR FILING DATE: 2001-10-15
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1997-03-19
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1997-03-19
PRIOR FILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: UP 63410/1996
PRIOR APPLICATION NUMBER: UP 63410/1996
PRIOR APPLICATION NUMBER: UP 69163/1997
PRIOR FILING DATE: 1997-03-19
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                                                                                                                                                                                                                                                                                                                                              137 H-----LCRCI--FGALHC---LPLQTPDRCDPKDFLASHAHGPS-----AGGAPSL 178
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                                                                             Gaps
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                        DB 7; Length 713;
                      Query Match
10.2%; Score 127.5; DB 7; Length 7
Best Local Similarity 25.3%; Pred. No. 0.00074;
Matches 55; Conservative 11; Mismatches 70; Indels
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; Sequence 34, Application US/10781841
; Selucation No. US20060134634A1
; GENERAL INFORMATION:
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US-11-183-325-56
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LENGTH: 810
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GENERAL INFORMATION:
APPLICANT: Vanderbilt University
APPLICANT: Vanderbilt University
APPLICANT: Vanderbilt University
APPLICANT: Vanderbilt University
ITILE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES
FILE REFERENCE: 1242/47/2/2 CIP
CURRENT APPLICATION NUMBER: US 60/328123
PRIOR APPLICATION NUMBER: US 60/328123
PRIOR APPLICATION NUMBER: US 60/328123
PRIOR PLING DATE: 2001-10-03
PRIOR PELING DATE: 2001-10-03
PRIOR PELING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin version 3.3
SEQ ID NO 56
LENGTH: 4391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/11264243
; Sequence 6, Application US/11264243
; Publication No. US20060134121A1
; GENERAL INFORMATION:
    APPLICANT: Thurston, Gavin
    APPLICANT: Gale, Nicholas
    APPLICANT: Object, Irene
    TITLE OF INVENTION: DLL4 Antagonists, Assays and Therapeutic
    TITLE OF INVENTION: Methods Thereof
    TITLE OF INVENTION: Methods Thereof
    TITLE OF INVENTION: Methods Thereof
    TITLE OF INVENTION NUMBER: US/11/264,243
    CURRENT FILING DATE: 2005-10-31
    PRIOR APPLICATION NUMBER: 60/623,658
    PRIOR PELING DATE: 2004-10-29
    NUMBER OF SEQ ID NOS: 17
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 6
    LENGTH: 2556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.8%; Score 123; DB 7; Length 4391; Best Local Similarity 27.3%; Pred. No. 0.013; Matches 39; Conservative 4; Mismatches 42; Indels 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 CIFGALHCLPLQTPDRCDPKDFLASHAHG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3937 SYLALPALTNTHHELRLDVEFKP 3959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 SLLLLLPCALLHRLLRPDAPAHP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: P98160
DATABASE ENTRY DATE: 2003-02-28
RELEVANT RESIDUES: (1)..(4391)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 46; Conserv
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1098 VPSAAAARLPLPATTSLGPAAVPLASLAPAA-SRDVRPGG 1136
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Pred. No. 0.0033;
8; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 LLHRLLRPDAPAHPRSLVPSVLQRERRPCG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 562 AVVVCVŘLKLOKH------ÓPPPEPČG 582
                                                                                                                                                                                                                                                                APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCarthy, Sean A.
APPLICANT: Gearing, David
APPLICANT: Holtzman, Douglas A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR PELLIANG DATE: 2003-07-07, 90 PRIOR PELLIANG DATE: 2003-04-17 PRIOR PELLIANG DATE: 2003-04-17 PRIOR PELLING DATE: 2003-04-17 PRIOR PELLING DATE: 2003-04-17 PRIOR PELLING DATE: 2000-05-09 PRIOR PELLING DATE: 1997-06-11 PRIOR PELLING DATE: 1997-04-04 PRIOR PELLING DATE: 1997-04-04 PRIOR PELLING DATE: 2004-07-21 PRIOR PELLING DATE: 2004-07-21 PRIOR PELLING DATE: 2002-03-25 PRIOR PELLING DATE: 2002-03-25 PRIOR PELLING DATE: 2002-05-22 PRIOR PELLING DATE: 2002-05-22 PRIOR PELLING DATE: 2002-05-22 PRIOR PELLING DATE: 1998-04-17 PRIOR PELLING DATE: 1997-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 195
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 720
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; Sequence 22, Application US/10669920
; Publication No. US20060194265A1
                                                                                                                                                              Sequence 4, Application US/11175714 Publication No. US20060122373A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Samantha J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.6%;
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Best Local Similarity 30.0
Matches 45; Conservative
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US-11-175-714-4
                                                                                                                                                                                                                                                                                                                                                                                                                   Pan, Yang
Busfield,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Remaining
NUMBER OF
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141 CIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLLLLLPCALLHRLLRPDAPAHPR 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Metalidhara Padigaru
APPLICANT: Metalidhara Padigaru
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
FILE REFERENCE: Cura 551 CIP
CURRENT APPLICATION NUMBER: 10/453,372
PRIOR PADLICATION NUMBER: 10/65,877
PRIOR FILING DATE: 2003-06-03
PRIOR FILING DATE: 2001-01-22
PRIOR PLILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR PLILING DATE: 2001-01-25
PRIOR PLILING DATE: 2001-01-25
PRIOR PLILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR PLILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR PLILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-36
PRIOR PRI
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                                                                1046 CT----CPQGYTGPNC--QNLVHWCDSSPCKNGG--
                                                                                                                                                                                                  1092 GLYCDVPSVSCEVAAQRQGVDVARLCQHGGL 1122
                                                                                                                                     201 SL---VPSV-----LQRE----RRPCGRPGL 219
                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/11217997
Publication No. US20060111561A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stacie (Casman) Navara
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David W. Anderson
Xiaojia (Sasha) Guo
Luca Rastelli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elma R. Fernandes
Richard A. Shimkets
Meera Patturajan
Vladimir Y. Gusev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Valerie L. Gerlach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48; Conservative
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ORGANISM: Homo sapiens
US-11-217-997-14
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Best Local Similarity
Matches 48; Conserva
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APPLICANT: Barnes, Thomas M.
APPLICANT: Mackay, Charles
APPLICANT: Mackay, Charles
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: DELTA3, FTHWA-070, TANGO129 AND INTEGRIN ALPHA SUBUNIT PROTEIN
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REPERENCE: MPIOS-0100MNIM
CURRENT APPLICATION NUMBER: 2005-07-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---APSLLLLLPCA 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449 CANGGICRDSVNDFSCTCPPGYTGKNCSAPVSRCEHAPCHNGA----TCHORGORYMCEC 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prior Application data removed - See File Wrapper or PALM.
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Gaps

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3629 gsvpg-aggwgpwgpwshcskscggglrsktracpopppoglgbycggpraggevcgalp 3687
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                                                                                                                                                                                                                                                                                                    87 RPRCCRNGGTCVLG---SFCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRAC---HLCR 140
                                                                                                                                                                                                                                                                                                                                                                                                                       141 CI--FGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLLLLPCALLHRLLRPDAPAH 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 AHFTGRYCEHDQRRSECGA-----LEHGAWTLRACHLCRCIFGALHCLPLQT---- 153
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                                                                                                                                                                                                                                                                                                                                       81; Gaps
                                                                                                                                                                                                                                           27;
                                                                                                                                                                              Length 2505;
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                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 150, Application US/10505928

Publication No. US2006008832A1

GENERAL INFORMATION:

APPLICATION NO. US2006008832A1

TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

FILE REFERENCE: 28967/39178

CURRENT APPLICATION NUMBER: US 10/10/505,928

CURRENT FILING DATE: 2004-08-27

PRIOR PLING DATE: 2004-08-27

PRIOR FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 866

SOFTWARE: PATENTIN 3.2
                                                                                                                                                                        Query Match
9.4%; Score 117.5; DB 6;
Best Local Similarity 29.4%; Pred. No. 0.023;
Matches 40; Conservative 12; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.4%; Score 117.5; DB 6; Best Local Similarity 26.6%; Pred. No. 0.053; Matches 55; Conservative 6; Mismatches 65;
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Sequence 10, Application US/11217997

Publication No. US20060111561A1

GENERAL INFORMATION:

APPLICANT: Valerie L. Gerlach

APPLICANT: Richard A. Shimkets

APPLICANT: Richard A. Shimkets

APPLICANT: Meera Patturajan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : : | | |
------VNECDSRPC 1016
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                         LENGTH: 2505
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-150
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US-10-505-928-150
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LENGTH: 5738
                                                                                                                     US-10-669-920-15
SEQ ID NO 15
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APPLICANT: Malandro, Marc S.
TITLE OF INNENTION:
FILE REFERENCE: 20366-066001
CURRENT FILING DATE: 2003-09-23
CURRENT APPLICATION NUMBER: US/10/669,920
CURRENT APPLICATION NUMBER: US 10/004,113
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 10/004,113
PRIOR FILING DATE: 2001-11-08
PRIOR PILING DATE: 2001-11-08
PRIOR PILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2002-02-7
PRIOR FILING DATE: 2002-02-7
PRIOR FILING DATE: 2002-02-7
PRIOR FILING DATE: 2002-12-17
                                            APPLICANT: MOLIES, DAYLEW.

APPLICANT: MAIDAGEO, MARC S.

TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REFERENCE: 2036-0660, 920
CURRENT APPLICATION NUMBER: US/10/669, 920
CURRENT FILING DATE: 2003-09-23
PRIOR PILING DATE: 2001-10-23
PRIOR PLING DATE: 2001-10-8
PRIOR APPLICATION NUMBER: US 10/052, 482
PRIOR PILING DATE: 2001-11-30
PRIOR PILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-20
PRIOR PILING DATE: 2001-11-20
PRIOR PILING DATE: 2001-0-27
PRIOR PILING DATE: 2002-0-27
PRIOR PILING DATE: 2002-12-17
PRIOR PILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.6%; Score 120.5; DB 6; Length Best Local Similarity 42.6%; Pred. No. 0.012; Matches 26; Conservative 4; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 15, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
                               APPLICANT: Morris, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 C 141
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TYPE: PRT
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US-10-669-920-15
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SOFTWARE: Patentin Ver. 3.3
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US-11-071-796A-22
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                                                                                                                                                                                          APPLICANT: Meal anong
APPLICANT: Maralidhara Padigaru
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
FILE REFERENCE: Cura 551 CIP
CURRENT APPLICATION NUMBER: 10/453,372
PRIOR PELICATION NUMBER: 10/65,877
PRIOR PELICATION NUMBER: 10/055,877
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR PELING DATE: 2001-01-22
PRIOR PELING DATE: 2001-01-19
PRIOR PELING DATE: 2001-01-19
PRIOR PELING DATE: 2001-01-23
PRIOR PELING DATE: 2001-01-24
PRIOR PELING DATE: 2001-01-24
PRIOR PELING DATE: 2001-01-24
PRIOR PELING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR PELING DATE: 2001-01-25
PRIOR PELING DATE: 2001-01-26
PRIOR PELING DATE: 2001-01-26
PRIOR PELING DATE: 2001-01-36
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001
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Best Local Similarity 28.6%; Pred. No. 0.0018;
Matches 42; Conservative 14; Mismatches 41; Indels 50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 LOTPDRCDPKDFLASHAHGPSAGGAPS 177
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Publication No. US20060111561A1
GENERAL INFORMATION:
APPLICANT: Valerie L. Gerlach
APPLICANT: Elma R. Fernandes
APPLICANT: Richard A. Shimkets
APPLICANT: Richard A. Shimkets
APPLICANT: Meera Patturajan
APPLICANT: Vadiamir Y. Gusev
APPLICANT: Velizar T. Tchernev
APPLICANT: Stacie (Casman) Navara
APPLICANT: Stacie (Assman) Navara
APPLICANT: Stacie (Assman) Navara
APPLICANT: Laojia (Sasha) Guo-
APPLICANT: Luca Rastelli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: CuraSeqList version 0.1 SEQ ID NO 10
Velizar T. Tchernev
David W. Anderson
Xiaojia (Sasha) Guo
Luca Rastelli
Mei Zhong
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ORGANISM: Homo sapiens
US-11-217-997-10
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112 RYCEHDQRRSECGALEHGAWTLRACHL-CRC-----IFGALHCL-----P 150
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Publication No. US20060140943A1
GENERAL INFORMATION,
BRIAN ROBERT
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: DALLMAN, MARGARET JANE
APPLICANT: LAMB, JONATHAN ROBERT
APPLICANT: HOYNE, GERARD FRANCIS
APPLICANT: HOYNE, GERARD FRANCIS
TITLE OF INVENTION: IMMUNOTHERAPY USING MODULATORS OF NOTCH SIGNALLING
FILE REFERENCE: 674525-2018
CURRENT APPLICATION NUMBER: PCT/GB03/03874
PRIOR FILING DATE: 2005-09-05
PRIOR PPLICATION NUMBER: GE 0220658.9
PRIOR PLILING DATE: 2002-09-05
NUMBER OF SEQ ID NOS: 27
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PAPLICANT: Muralidhara Padigaru

APPLICANT: Muralidhara Padigaru

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
FILE REPREBRENCE: Cura Sil CIP

CURRENT APPLICATION NUMBER: 10/453,372

FRICA PAPLICATION NUMBER: 10/55,877

FRICA PAPLICATION NUMBER: 60/262,892

FRICA PAPLICATION NUMBER: 60/262,892

FRICA PALLON DATE: 2001-01-12

FRICA PLING DATE: 2001-01-13

FRICA PLING DATE: 2001-01-23

FRICA PLING DATE: 2001-01-24

FRICA PAPLICATION NUMBER: 60/264,117

FRICA PLING DATE: 2001-01-24

FRICA FLING DATE: 2001-01-24

FRICA FLING DATE: 2001-01-25

FRICA PAPLICATION NUMBER: 60/264,117

FRICA FLING DATE: 2001-01-25

FRICA FLING DATE: 2001-01-25

FRICA FLING DATE: 2001-01-26

FRICA FLING DATE: 2001-01-26

FRICA FLING DATE: 2001-01-26

FRICA FLING DATE: 2001-01-36

FRICA FRICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 LQTPDRCDPKDFLASHAHGPSAGGAPS 177
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                                                                                                                                                                                                                                                                                                                  93 GASARPRCCRNGGTCVL----GSFCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRAC 136
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CURRENT APPLICATION NUMBER: US/11/217,997
CURRENT FILING DATE: 2005-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - See File Wrapper or PALM. WUMBER OF SEQ ID NOS: 62 SOFTWARE: CuraSeqList version 0.1 SEQ ID NO 8
                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                                                           Length 2556;
                                                                                                                                                                                                                                                                                                                                                                                                                                             34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            137 HLCRCIFG----ALHCLPLQTPDRCDPKDFLASHAHGPSAGGAP 176
                                                                                                                                                                                                                      Score 115.5; DB 7;
Pred. No. 0.035;
                                                                                                                                                                                                                                                                     6; Mismatches
                                                                                                                                                      ; OTHER INFORMATION: Variable amino acid
US-11-071-796A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2005-08-31
PRIOR APPLICATION NUMBER: 10/453,372
PRIOR APPLICATION NUMBER: 10/055,877
PRIOR PILING DATE: 2003-06-03
PRIOR PILING DATE: 2002-01-22
PRIOR PILING DATE: 2001-01-39
PRIOR FILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-33
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR PILING DATE: 2001-01-25
PRIOR PELING DATE: 2001-01-26
PRIOR PILING DATE: 2001-01-36
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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Richard A. Shimkets
Meera Patturajan
Vladimir Y. Gusev
Stacie (Casman) Navara
Velizar T. Tchernev
David W. Anderson
Xiaojia (Sasha) Guo
Luca Rastelli
Mei Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/11217997
Publication No. US20060111561A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                      9.2%;
                                                                                                                                                                                                                                                Best Local Similarity 35.69
Matches 37; Conservative
                     LENGTH: 2556
TYPE: PRT
ORGANISM: Homo sapiens
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US-11-217-997-8
                                                                                    FEATURE:
NAME/KEY: MOD RES
LOCATION: (891)
SEQ ID NO 22
                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 -----HLCRCI--FGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLL----LLLLP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               406 CVEGGGAHRCSCALGFGGRDC----RERADP-----CARPCAHGGRCYAHFSGLVCA 454
                                                                                                                                                                                   30 IPASARTEĠPVTLSQACEHPCPPG---FHĠAGRQGLCWCOHĠAPCDPISGRCLCPAGFHĠ
                                                                                                                        61 VTGSAEGWGP-----EEPLPYSRAFGEGASARPRC-CRNGGTC-VLGSFCVCPAHFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356 RCSLQPCRNGGLCLDLGHALRCRCRAGFAGPRCEHD--LDDCAG------RACANGGT
                                                                    50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Edmonds, Brian
APPLICANT: Edmonds, Radmila
APPLICANT: Micanovic, Radmila
APPLICANT: Ou, Weijia
APPLICANT: Su, Bric
APPLICANT: Trchnng, Sheng-Hung
APPLICANT: Wang, He
TITLE OF INVENTION: Novel secreted proteins and their uses
FILE REFERENCE: X-14001
CURRENT APPLICATION NUMBER: US/11/030,653
CURRENT FILING DATE: 2005-01-06
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 32
LENGTH: 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOS-11-178-724-19
Sequence 19, Application US/11178724
Sequence 19, Application US/11178724
Sequence 19, Application US/11178724
Sequence 19, Application US/011178724
GENERAL INFORMATION:
APPLICANT: CHAMPION, BRIAN R.
APPLICANT: YOUNG, LESLEY L.
APPLICANT: YOUNG, LESLEY L.
TITLE OF INVENTION: THERAPEUTIC USE OF MODULATORS OF NOTCH
FILE REFREENCE: 674525-2021
CURRENT APPLICATION NUMBER: US/11/178,724
CURRENT FILING DATE: 2005-07-11
PRIOR APPLICATION NUMBER: PCT/GB04/00021
PRIOR FILING DATE: 2004-01-09
PRIOR FILING DATE: 2003-01-09
Query Match
9.2%; Score 115; DB 7; Length 170;
Best Local Similarity 28.6%; Pred. No. 0.0024;
Matches 42; Conservative 14; Mismatches 41; Indels
                                                                                                                                                                                                                                                        112 RYCEHDORRSECGALEHGAWTLRACHL-CRC-----IFGALHCL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.2%; Score 114.5; DB 7; Best Local Similarity 31.6%; Pred. No. 0.0095; Matches 50; Conservative 8; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                 151 LQTPDRCDPKDFLASHAHGPSAGGAPS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                     138 LRLPEN-----PSLAQG-SAGTLPA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32, Application US/11030653 Publication Nd. US20060147945A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-11-030-653-32
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13;
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                                                                                                                                                                                                                       137 -----HLCRCI--FGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLL----LLLP 183
                                                                                                                                                                                                                                                                                             406 CVEGGGAHRCSCALGFGGRDC-----RERADP-----CAARPCAHGGRCYAHFSGLVCA 454
                                                                                                                                                                     55; Gaps
                                                                                                                                 Query Match
9.2%; Score 114.5; DB 7; Length 618;
Best Local Similarity 31.6%; Pred. No. 0.01;
Matches 50; Conservative 8; Mismatches 45; Indels 55.
                                                                                                                                                                                                                                                                                                                                    ; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 19
; LENGTH: 618
; TYPE: PRT
; ORCANISM: Homo sapiens
US-11-178-724-19
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Search completed: September 7, 2006, 12:15:34 Job time: 34 secs

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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                       Copyright
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29-JUL-2004

ADO05060;

- protein search, using sw model OM protein

Seconds 7, 2006, 12:15:10 ; Search time 191 September е Е Run

(without alignments) 533.818 Million cell updates/sec

US-10-665-602-2

223 1 MTWRHHVRLLFTVSLALQII.......PSVLQRERRPCGRPGLGHRL 223 Perfect score:

Sequence:

OLIGO Gapop 60.0 , Gapext Scoring table:

2589679 seqs, 457216429 residues Searched:

30

Total number of hits satisfying chosen parameters: Word size :

15

seq length: 0 seq length: 200000000 88 Minimum Maximum summaries Post-processing: Listing first 45

Genesed 8:\* Database

geneseqp1980s:\*
geneseqp2000s:\*
geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2001s:\*
geneseqp2003as:\*
geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:\*

# SUMMARIES

	lon	Human cri	Novel hum	Human nov		Novel	Novel hum	Human pol	Human pol	Lung canc	Cancer/an	Cancer/an	_	Human nov	Human cri	Human cry
	Description	Ado05060	Aau18122	Aau17028	Abb10300	Aau19904	Abj05749	Abp66887	Abb90336	Abu56711	Adn39104	Adn39975	Ady85963	Aau16957	Aaw09111	Aag77914
	ID	ADO05060	AAU18122	AAU17028	ABB10300	AAU19904	ABJ05749	ABP66887	ABB90336	ABU56711	ADN39104	ADN3 9975	ADY85963	AAU16957	AAW09111	AAG77914
	DB	60	4	4	4	4	Ŋ	Ŋ	Ŋ	9	7	7	σ	4	7	ß
	Query Match Length DB	223	229	229	229	229	229	229	223	223	223	223	223	231	230	223
de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	.100.0	83.9	83.9	83.9	83.9	83.9	83.9	66.8	65.0
	Score	223	223	223	223	223	223	223	187	187	187	187	187	187	149	145
	Result No.	-	7	m	4	S	y	7	α0	O	10	11	12	13	14	15

### ALIGNMENTS

RESULT 1 ADO05060 ID AD005060 standard; protein; 223 AA.

Criptin growth factor; CGF; wound healing; tissue regeneration; implant fixation; angiogenesis; neoplasia; tumour; gene therapy; human. New human polynucleotides encoding human criptin growth factor polypeptides, useful for wound healing or tissue regeneration, stimulating implant fixation and angiogenesis, and for treating and/or Human criptin growth factor (CGF) protein. 95US-00471371. 99US-00393023. (HUMA-) HUMAN GENOME SCI INC 22-SEP-2003; 2003US-00665602 Coleman TA; WPI; 2004-356201/33 preventing tumor. N-PSDB; AD005059 US2004086967-A1. 06-JUN-1995; Meissner PS, 06-MAY-2004 

The invention provides criptin growth factor (CGF) polypeptides and their encoding polynucleotides. The invention is useful for wound healing and tissue regeneration, stimulating implant fixation, angiogenesis and for treating and preventing neoplasia such as tumour. The invention is also useful in gene therapy. The present sequence is human criptin growth factor (CGF) protein. Claim 12; SEQ ID NO 2; 19pp; English.

Sequence 223 AA;

ö 1 MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE Gaps ö Length 223; Indels 100.0%; Score 223; DB 8; L. Ilarity 100.0%; Pred. No. 1.4e-195; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches 223; Conserv Best Loca Matches ò

120 61 VIGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR 120 9 1 MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE 61 VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR 용 ò 셤

180 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL ò g

LLPCALLHRLLRPDAPAHPRSLVPSVLQRERRPCGRPGLGHRL 223 181 181 셤 Š

AAU18122 standard; protein; 229 AAU18122; RESULT 2 AAU18122 SAXAXEX

21-NOV-2001 (first entry)

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2000US - 0234223P

2000US - 0234924P

2000US - 023498P

2000US - 0235484P

2000US - 0235484P

2000US - 0235377P

2000US - 0235377P

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29-SEP-2000

29-SEP-2000

29-SEP-2000

29-SEP-2000

29-SEP-2000

29-SEP-2000

20-OCT-2000

20-OC
   Human; uterine motility-association disorder; uterus; pregnancy; labour; menstrual cycle; gene therapy.
   human uterine motility-association polypeptide #29
                                                                                                                                                                                                                       2000US-0139065P

2000US-0186628P

2000US-0189814P

2000US-0199014P

2000US-01990176P

2000US-01990176P

2000US-0215135P

2000US-02148880P

2000US-0214887P

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2000US-021498P

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2000US-021498P

2000US-021498P

2000US-02149P

2000US-022526P

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2000US-02394P

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2000US-02394P
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2000US-0232400P.
2000US-0232401P.
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2000US-0233064P.
2000US-0233065P.
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                                                                                                                       WO200155201-A1
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                                                                                       Homo sapiens
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   Novel
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17-JAN-2001; 2001WO-US001320
                   WO200155441-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-AUG-2000;
   The present invention relates to the isolation of novel human uterine motility-association polypeptides, and cDNA (AAS28936-AAS28994) and genomic sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with uterine motility such as pregnancy and labour, and menstrual disorders. The polymucleotide sequences of the invention are also useful in gene therapy. AAU18094 AAU18152 represent novel human uterine motility-association polypeptides. Note: The sequence was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; unlnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardia arthritis; hyperproliferative disorder; cardiovascular disorder; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDORR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFIGRYCEHDQRR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 MTWRHYVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE 66
                                                                                                                                                                                 New nucleic acid molecules encoding 49 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 223; DB 4; I
100.0%; Pred. No. 1.5e-195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human novel secreted protein, SEQ ID 269.
                                                                                                                                                                                                                                                    Claim 11; SEQ ID NO 98; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU17028 standard; protein; 229 AA
                                                                                                 Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiproliferative
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                                (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 223; Conservative
                                                                                               Barash SC,
                                                                                                                                 2001-488777/53.
                                                                                                                                                    N-PSDB; AAS28964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 229 AA;
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                                                                                                 Rosen CA,
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08-NOV-2000; 2000US-0246532P.
08-NOV-2000; 2000US-0246532P.
08-NOV-2000; 2000US-0246609P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-0246611P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-024924P.
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17-NOV-2000; 20000S-0249297P.
17-NOV-2000; 20000S-0249299P.
17-NOV-2000; 20000S-0249300P.
01-DEC-2000; 2000US-025919P.
01-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025198P.
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20000S-0239937P.
20000S-0241281P.
20000S-0241787P.
20000S-024186P.
20000S-024186P.
20000S-0244617P.
20000S-0246417P.
20000S-0246417P.
20000S-0246417P.
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20000S-0246417P.
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2000US-023630P

2000US-0236302P

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08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251989P.
                                        2000US-0236367P
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29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-SEP-2000; 20-SE
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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in allating symptoms associated with the disorders and in diagnostic (ELISA). Disorders which are diagnosed or treated include autoimmune (ELISA). Disorders which are diagnosed or treated include autoimmune (ELISA). Disorders which are diagnosed or treated include autoimmune (C apsease e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiacd arrest, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to regenerate tissues and in chemotaxis. The polypeptides can also be used craspalnitive or preservative to increase or decrease storage craspabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present expensents a novel secreted protein of the invention. Note: The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                              Novel polypeptides and polynucleotides useful as diagnostic reagents t diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 LLPCALLHRLLRPDAPAHPRSLVPSVLQRERRPCGRPGLGHRL 229
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                                                                                                                                                                                                                                          Claim 11; SEQ ID NO 269; 601pp; English
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Ruben SM;
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Barash SC,
                                               2001-476222/51.
                                               WPI; 2001-476222
N-PSDB; AAS26933
                                                                                                                                                                                          nemophilia.
Ковеп СА,
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(HUMA-) HUMAN GENOME SCI INC

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2000US-0236327P

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29-SEP-2000;
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    31-JAN-2000) 2000US-0119065P.
24-PAR-2000) 2000US-0118645P.
02-PAR-2000) 2000US-0118645P.
02-PAR-2000) 2000US-0118645P.
11-MAR-2000) 2000US-0118645P.
11-MAR-2000) 2000US-01189874P.
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11-JUL-2000) 2000US-011888P.
11-JUL-2000) 2000US-01188P.
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11-JUL-2000) 2000US-0118BP.
11-SEP-2000) 
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                          WO200154474-A2
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2000US-0225757P.
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2000US-0225759P.
2000US-0226279P.
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2000US-0224519P.
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114-SEP-2000;
14-SEP-2000;
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14-AUG-2000;
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18-AUG-2000;
22-AUG-2000;
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23-AUG-2000;
30-AUG-2000;
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14-AUG-2000;
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01-SEP-2000;
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67 VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR 126
                                                                                                                                                                                                                                                                                                                                                          SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 186
                                                                                                                                                                                                                                                                                                VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR 120
                                                                                                                                                                                                                                                                                                                                            SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPXDFLASHAHGPSAGGAPSLLL 180
                                                                                                                   The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                         MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE
                                                                                                                                                                                                                                                        MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE
                                                     Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; calcium-binding protein; calcium flux; neurological disease;
immune dysfunction; digestive disorder; neoplastic disease;
blood disorder; infectious disease; gene therapy; immunosuppresive;
antiarthritic; cytostetic; vasotropic; antibacterial; nootropic;
                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                             Length 229;
                                                                                                 Claim 11; SEQ ID NO 608; 859pp + Sequence Listing; English
                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                 0; Mismatches
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  Ruben SM;
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04-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0184564P.
16-MAR-2000; 2000US-018974P.
17-MAR-2000; 2000US-0199123P.
18-APR-2000; 2000US-019132P.
19-MAY-2000; 2000US-019123P.
07-JUN-2000; 2000US-0205515P.
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                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 223; Conservative
Barash SC,
                     WPI; 2001-476161/51
N-PSDB; ABA06522.
                                                                                                                                                                                       Sequence 229 AA;
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                                                                           condition.
  Rosen CA,
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The present invention relates to the isolation of novel human calciumbinding proteins, and cDNA (AAS31577-AAS31654) and genomic sequences encoding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. amylotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecule encoding a calcium-binding protein is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 101; 542pp; English
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                                     2000US-0241826P.
2000US-0244617P.
2000US-0246474P.
2000US-0246475P.
2000US-02464776P.
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2000US-0249209P.
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2000US-0249297P.
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N-PSDB; AAS31589.
        20-0CT-2000;
20-0CT-2000;
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01-00V-2000;
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08-DEC-2000; 2
08-DEC-2000; 2
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combined immunodeficiency, SCID), digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders (e.g. hamophilia), and/or infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit activities mediated by calcium-binding proteins. The polynucleotides of the invention are also useful in gene therapy. AAU19892-AAU1996 represent the novel human calcium-binding proteins. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunostimulant; antirheumatic; antiarthritic; neuroprotective; antiallergic; antidiabetic; antiasthmatic; antinflammatory; nootropic; immunosuppressive; anticoagulant; thrombolytic; antiatherosclerotic; cytostatic; nephrotropic; antiparkinsonian; gynecological; virucide; antibacterial; antiarrhythmic; fungicide; HCFATO5; HMAABS5; HTNBM01; immunodeficiency; autoimmune disorder; allergic reaction; cardiovascular; inflammatory condition; graft-versus-host disease; reproductive system; blood-related disorder; hyperproliferative; endocrine; neurological; respiratory; renal; infectious disease; gastrointestinal; gene therapy; neuronal growth; neuronal disorder; neuro-degenerative condition;
                                                                                                                                                                                                                                                                                                                                                                                                              VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
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2000US-0216880P.
2000US-0217487P.
2000US-0217496P.
2000US-0218290P.
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2000US-0214886P
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Matches 223; Conservative
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28-JUN-2000;
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Disclosure; Page 268-269; 335pp; English
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14-AUG-2000) 2000US-0225267P.
14-AUG-2000) 2000US-0225270P.
14-AUG-2000) 2000US-0225757P.
14-AUG-2000) 2000US-0225757P.
14-AUG-2000) 2000US-0225987P.
01-SEP-2000) 2000US-022987P.
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07-CT-2000) 2000US-023969P.
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RUBEN S M.
BARASH S C.
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Novel polypeptide useful for diagnosis, prognosis, prevention, and treatment of immune, hyperproliferative, renal, respiratory, cardiovascular, reproductive, endocrine, gastrointestinal and neurological disorders.

The invention relates to an isolated polypeptide comprising a sequence at least 90% identical to a full length protein sequence selected from 55 sequences given in the specification such as a sequence of 163, 74 or 140 amino acids fully defined in the specification, or the encoding sequence contained in 49 cDNA clones given in specification e.g. HCRATOS, HWAAES5 or HTMBNOI. The protein and its encoding nucleic acid are useful for disgnosing a pathological condition or susceptibility to a pathological condition in a subject and for preventing, treating or ameliorating a macical condition. The protein, its encoding nucleic acid and an isolated antibody that can bind to the protein are useful in treating, preventing, diagnosing and/or prognosing immunodeficiencies, autoimmune disorders, allergic reactions and conditions, inflammatory conditions, graft versushost classes, blood related disorders, hyperproliferative disorders, renal disorders, cardiovascular disorders, respiratory disorders, neurological disorders, endocrine disorders, reproductive system

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disorders, infectious diseases, and gastrointestinal disorders. The protein of the invention is useful to stimulate neuronal growth and to netreat, prevent, and/or diagnose neuronal damage which occurs in certain neuronal disorders or neuro-degenerative conditions, for stimulating keratinocyte growth, to prevent hair loss, to modulate mammalian characteristics such as body height, weight, hair color, and to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. The nucleic acid of the invention can be used in gene therapy. This sequence represents a novel human protein of the invention
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                                                                                                                                                                                                                                                                        1 MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE
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Best Local Similarity
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14-JUL-2000;
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28-JUN-2000;
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VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR 67 VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR

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Gaps

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Length 229; Indels

100.0%; Score 223; DB 5; L 100.0%; Pred. No. 1.5e-195; iive 0; Mismatches 0;

Query Match Best Local Similarity 100.' Matches 223; Conservative

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1 MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE 7 MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE LLPCALLHRLLRPDAPAHPRSLVPSVLQRERRPCGRPGLGHRL 223

ABB90336 standard; protein; 223 AA

RESULT 8 ABB90336 Human polypeptide SEQ ID NO 2712.

24-MAY-2002 (first entry)

ABB90336;

SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPXDFLASHAHGPSAGGAPSLLL

121

181 187

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14-MUG-2000; 2000US-0225758P.
22-AUG-2000; 2000US-0228954P.
01-SEP-2000; 2000US-0228934P.
01-SEP-2000; 2000US-0229343P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229344P.
05-SEP-2000; 2000US-0229513P.
05-SEP-2000; 2000US-0229513P.
21-SEP-2000; 2000US-023422P.
21-SEP-2000; 2000US-023422P.
21-SEP-2000; 2000US-023423P.
21-SEP-2000; 2000US-023423P.
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02-OCT-2000; 2000US-0236370P.
02-OCT-2000; 2000US-023703PP.
02-OCT-2000; 2000US-023703PP.
02-OCT-2000; 2000US-023703PP.
13-OCT-2000; 2000US-023903P.
20-OCT-2000; 2000US-023903P.
20-OCT-2000; 2000US-024178SP.
20-OCT-2000; 2000US-024180P.
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08-DEC-2000; 2000US-0251869P
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                                                                                                                                                                                                                                                                                                                (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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29-SEP-2000; 2
29-SEP-2000; 2
29-SEP-2000; 2
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Novel polypeptide useful for diagnosis, prognosis, prevention, treatment of immune, hyperproliferative, renal, respiratory, cardiovascular, reproductive, endocrine, gastrointestinal and neurological disorders.

Claim 11, SEQ ID NO 608; 369pp + Sequence Listing; English.

The invention relates to novel genes (ABV83682-ABV84101) and proteins (ABP66710-ABP67129) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tisques disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections by such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not format directly from MIPO at ftp.wipo.int/pub/published\_pct\_sequences

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Sequence 229

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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune basonismune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
                                                                                                                                                  Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
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WPI; 2002-122018/16.
N-PSDB; ABL90745.
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidecterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein. 18-MAY-2001; 2001WO-US016450. 19-MAY-2000; 2000US-0205515P. (HUMA-) HUMAN GENOME SCI INC Birse CE, Rosen CA; WO200190304-A2. Homo sapiens. 29-NOV-2001

and

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Lung cancer-associated polypeptide, cytostatic, emphysema; atelectasis, antinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lession; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
cardiovascular disorders such as myocardial ischaemias; (d) wound healing ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                           CDPKDFLASHAHGPSAGGAPSLLLLLPCALLHRLLRPDAPAHPRSLVPSVLQRERRPCGR 216
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                                                                                                                                                                                                                              EVTKVATQKHRQSPLNWTSSHFGEVTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGT
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                                                                                                                                           83.9%; Score 187; DB 5; Length 223; 100.0%; Pred. No. 1.3e-162; ive 0; Mismatches 0; Indels
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10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-0339245P.
13-NOV-2001; 2001US-03350666P.
29-NOV-2001; 2001US-033470P.
12-APR-2002; 2002US-0372246P.
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N-PSDB; ABX76440.
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Best Local Similarity
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological cample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibite to a sequence that is at least 80 % identical to a gene that exhibite concerned or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated polypeptide, for cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, or other benign or precancerous lessions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary disease, fibrosis, bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences
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100.0%; Pred. No. 1.3e-162;
ive 0; Mismatches 0;
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Claim 27; Page 426; 453pp; English
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21-NOV-2001; 2001US-0332464P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 223 AA;
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Matches
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Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO: C345.
 ADN39975 standard; protein; 223 AA.
                                                               17-JUN-2004 (first entry)
   The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or other diseases auch as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; colypeptides and nucleic acids. The nucleic acids, polypeptides, cand methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, anterimental and cher conditions such as psoriasis, ischaemia, retinal neovascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                      Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
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E, Zlotnik A;
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Wilson KE,
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R, Watson SR,
03-DEC-2001; 2001US-0335394P.

14-DEC-2001; 2001US-0340376P.

08-JAN-2002; 2002US-0347319P.

10-JAN-2002; 2002US-0347349P.

18-FEB-2002; 2002US-0355250P.

13-FEB-2002; 2002US-035514P.

20-FEB-2002; 2002US-0359077P.
                                                                                                                                                                                                                                                             (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                             29-MAR-2002; 2002US-0368809P.
04-ARPR-2002; 2002US-0370IIOP-
12-ARP-2002; 2002US-0372246P.
05-JUN-2002; 2002US-0386614P.
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Murray R,
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Mack DH,
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PGLGHRL 223

RESULT 11

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The invention relates to nucleic acids and proteins (ADN38681-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
cother diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
nucleic acid of the invention; use of such antibodies for drug targeting;
onlypeptides of screening for modulators of activity or expression of the
polypeptides and nucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularistaion syndromes, scarring and uterine fibroids. They may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
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Wilson KE, Zlotnik A;
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Murray R, Watson SR,
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2001US-0332464P.
2001US-0334393P.
2001US-0335394P.
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2002US-0356714P.
2002US-0359077P.
2002US-0368809P.
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2002US-0347211P.
2002US-0347349P.
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2002US-0386614P.
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N-PSDB; ADN39758.
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2000US-0216647P
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                                                                                                                   Sequence 223 AA,
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02-MAR-2000;
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Best Local 9
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                                                                                                                                                                     This invention relates to a novel method for augmenting signaling of a ligand of a receptor serine kinase within a cell by inhibiting the formation of complexes between Cripto and this ligand on the surface of the cell. Specifically, it refers to TGF-beta and activin which are the ligands of serine kinase receptors and which regulate tissue homeostasis by activating the Smad2/3 intracellular signaling pathway; disruption of this signaling pathway is associated with oncogenesis and tumorigenesis. As such, the present invention describes a method for augmenting Smad2/3 signaling in a cell by administering a mutant ligand that retains signaling activity but is unable to bind to Cripto, and thus bypasses antagonism by Cripto. Note that augmentation of signaling increases phosphorylation and activation of Smad2 and Smad3 in the cell, such that
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                                                                                                                                                                                                                                                                                                                                                                                                                                  oncogenesis; antisense therapy; cytostatic; mutagenesis;
                                                                                                                                                      CVLGSFCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR
                                                                                                        EVTKVATQKHRQSPLNWTSSHFGEVTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGT
                                                                                                                               EVTKVATOKHROSPLNWTSSHFGEVTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGT
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                                                                                  Gaps
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contraception. The present
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0
                                                         Length 223;
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                                                                               Indels
also be useful in wound healing and in contraceptio sequence represents a polypeptide of the invention.
                                                         Score 187; DB 7; Le
Pred. No. 1.3e-162;
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                                                 83.9%; Scor.
100.0%; Pred. No. 1...
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gray PC, Harrison CA;
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                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                 Matches 187; Conservative
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                                                                    Local Similarity
                                  Sequence 223 AA
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it decreases the proliferative rate of the cell. The receptor serine kinase is a type I activin receptor-like kinases-4 or -5 (ALK-4 or ALK-5) and the formation of complexes is inhibited by suppressing expression of Cripto using antisense oligomoucleotides (siRNA) directed against Cripto, and also mutating at least one allele of Cripto by homologous ercombination. Accordingly, pharmaceutical compositions derived thereof exhibit cytostatic activity. This polypeptide sequence is the human Criptic protein, a member of the EGF-CFC (Epidermal Growth Factor-Cripto, FRL-1, Criptic) family of proteins of the invention.
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Pred. No. 1.3e-162;
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100.0%; Pred. No. ...
0; Mismatches
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2000US-0198123P.
2000US-0205515P.
2000US-0214886P.
2000US-0214886P.
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2000US-0184664P.
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07-JUL-2000; 2000US-02168B0P.

11-JUL-2000; 2000US-0211748PP.

11-JUL-2000; 2000US-0211748PP.

14-JUL-2000; 2000US-0211748PP.

14-JUL-2000; 2000US-0212990P.

14-JUC-2000; 2000US-022594PP.

14-JUC-2000; 2000US-022526PP.

14-JUC-2000; 2000US-022529PP.

14-JUC-2000; 2000US-022529PP.

14-JUC-2000; 2000US-022529PP.

14-JUC-2000; 2000US-022539PP.

14-JUC-2000; 2000US-022539PP.

14-JUC-2000; 2000US-022339PP.

14-SEP-2000; 2000US-022339PP.

14-SEP-2000; 2000US-022339PP.

14-SEP-2000; 2000US-023339PP.

14-SEP-2000; 2000US-023339PP
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2000US-0244617P 2000US-0244617P 2000US-0246476P 2000US-0246477P 2000US-0246477P 2000US-0246524P 2000US-0246524P 2000US-0246524P 2000US-0246524P 2000US-0246524P 2000US-0246524P 2000US-0246521P 2000US-0246521P 2000US-024651P 2000US-0249201P 2000US-0249201P 2000US-0249211P 2000US-0250160P 2000US-0250160P 2000US-0250180P 2000US-02511868P 2000US-02511869P 2000US-02511869P 05-JAN-2001; 2001US-0259678P 20 - OCT - 2000;
20 - OCT - 2000;
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80 - NOV - 2000;
81 - N 17-NOV-2000; 2 01-DEC-2000; 2 01-DEC-2000; 2 05-DEC-2000; 2 05-DEC-2000; 2 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 06-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 

(HUMA-) HUMAN GENOME

Ruben SM Barash SC, ð Rosen

WPI; 2001-476222/51. N-PSDB; AAS26862.

S Novel polypeptides and polynucleotides useful as diagnostic reagents that diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, hemophilia.

Claim 11; SEQ ID NO 198; 601pp; English

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic

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immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays

(ELISA). Disorders which are diagnosed or treated include autoimmune
diseases e.g. rheumatoid arthritis, hyperpoilferative disorders e.g.
cliseases e.g. rheumatoid arthritis, hyperpoilferative disorders e.g.
neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
arrest, cerebrovascular disorders e.g. cerebral ischaemia, andiogenesis,
nervous system disorders e.g. Alzheimer's disease, infections caused by
and many other disorders listed in the specification. The polypeptides
can also be used to aid wound healing and epithelial cell proliferation,
to prevent skin aging due to sumburn, to maintain organs before
transplantation, for supporting cell culture of primary tissues, to
regenerate tissues and in chemotaxis. The polypeptides can also be used
as a food additive or preservative to increase or decrease storage
capabilities, fat content, lipid, protein, carbohydrate, vitamins,
minerals, cofactors and other nutritional components. The present
sequence represents a novel secreted protein of the invention. Note: The
                                                                                                                                                                                                                                                                                                                                                                                                                                           CVLGSFCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVLGSFCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 164
                                                                                                                                                                                                                                                                                                                                                                                                        EVTKVATOKHROSPLNWTSSHFGEVTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDPKDFLASHAHGPSAGGAPSLLLLLPCALLHRLLRPDAPAHPRSLVPSVLQRERRPCGR 216
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0
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/label- Sig_peptide
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N-PSDB; AAT51058.
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                                                                                            Human criptin growth factor (CGF) (AAW09111) is a novel polypeptide structurally related to human cripto growth factor. It is overexpressed and secreted by certain types of cancer cells, e.g. pancreatic cancers. Recombinant CGF can be produced in host cells utilising vectors incorporating a CGF CDNA clone (AATS1058) isolated from a human pancreatic cancer tissue cDNA library. CGF can be used to treat e.g. muscle wasting diseases, osteoporosis, to aid implant fixation, to stimulate tissue regeneration and wound healing, to promote angiogenesis and to stimulate proliferation of vascular smooth muscle and endothelial cell prodn. It can also be used as a marker for cancer diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                    96
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v isolated human Criptin Growth Factor polypeptide - which can be used stimulate angiogenesis and develop products for use in diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cryptic; human; cytostatic; cardiant; nootropic; neuroleptic; cancer; antiasthmatic; anti-anglogenic; gene therapy; lung cancer; asthma; respiratory disease; epilepsy; schizophrenia; depression; hyperactivity; heart hypertrophy; heart failure; cardiomyopathy; anglogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel cryptic-like secreted polypeptide found in various tumors and organs is useful to treat diseases including cancer, particularly lung cancer, asthma and heart disease.
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100.0%; Pred. No. 8.1e-128;
ive 0; Mismatches 0;
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                                                                Claim 12; říg 1; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cryptic-like polypeptide.
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Matches 149; Conservative
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The sequence represents the novel human cryptic-like secreted protein of the invention. The polypeptide of the invention has cyrostatic, cardiant, nootropic, neuroleptic, antiasthmatic, and anti-angiogenic activity, and has a use in gene therapy. The polypeptide and polymucleotide of the invention may be used to treat cancer, particularly lung cancer, respirancy diseases, asthma, epilepsy, schizophrenia, depression, hyperactivity, heart hypertophy, heart failure, cardiomyopathies, aberrant angiogenesis and vasculogenesis
Claim 1; Page 33-34; 37pp; English
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Sequence 223 AA;

ö 79 AFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRACHL 138 0; Gaps Length 223; Query Match 65.0%; Score 145; DB 5; Length 223 Best Local Similarity 100.0%; Pred. No. 3.6e-124; Matches 145; Conservative 0; Mismatches 0; Indels 199 PRSLVPSVLQRERRPCGRPGLGHRL 223 199 g 요 ò ò ઠે g

Search completed: September 7, 2006, 12:18:51 Job time : 192 secs

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SECTION CHARTON

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

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(without alignments) 520.200 Million cell updates/sec

US-10-665-602-2 1249 Perfect score:

1 MTWRHHVRLLFTVSLALQII........PSVLQRERRPCGRPGLGHRL 223

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

2589679 segs, 457216429 residues Searched:

2589679 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Genesed 8: Database

geneseqp1990s:\* geneseqp2000s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2001s:\* geneseqp2003bs:\* geneseqp2003bs:\* geneseqp2006s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

139 8 ADS88694 190 2 AAR90768 360 5 ABR77107 367 5 ABB77106 188 2 AAW29735 1129 5 ABB77104 1139 5 ABB77104 1139 5 ABB77104 1139 5 ABB77104 1134 2 AAW32107 114 2 AAW32107 115 8 ADO88699 1188 2 AAW32107 1188 2 AAW37101 1188 5 AAO14638 1188 5 AAO14638 1188 5 AAO14638 1188 5 AAO14636 1188 6 AAP58131	Ads88694 Sequence	Ady85964 African c	Aar90768 FGF recep	Abb77107 Human Cri	Abb77106 Human Cri	Aaw29735 Homo sapi	Ads88697 Amino aci	Abb77104 Human Cri	Abb77103 Human Cri	Ads88698 Amino aci	Aar13326 Recombina	Aaw32107 Recombina	Ado05065 Human cri	Ads88699 Amino aci	Aar22548 Human CRI	Aaw87630 Human CRI	Abb77101 Human Cri	Aao14638 Human cri	Aao14636 Human cri	Aao14727 Human var	Abp97176 Tumour-as	Abp58131 Human Cri
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## ALIGNMENTS

Criptin growth factor; CGF; wound healing; tissue regeneration; implant fixation; angiogenesis; neoplasia; tumour; gene therapy; human. Human criptin growth factor (CGF) protein. AD005060 standard; protein; 223 AA. 95US-00471371. (HUMA-) HUMAN GENOME SCI INC. 22-SEP-2003; 2003US-00665602 (first entry) Coleman TA; US2004086967-A1. Homo sapiens. 06-JUN-1995; 09-SEP-1999; Meissner PS, 29-JUL-2004 06-MAY-2004. ADO05060; 

WPI; 2004-356201/33. N-PSDB; ADO05059 New human polynucleotides encoding human criptin growth factor polypeptides, useful for wound healing or tissue regeneration, stimulating implant fixation and angiogenesis, and for treating and/or preventing tumor

Claim 12; SEQ ID NO 2; 19pp; English.

The invention provides criptin growth factor (GGF) polypeptides and their encoding polynucleotides. The invention is useful for wound healing and tissue regeneration, stimulating implant fixation, angiogenesis and for treating and preventing neoplasia such as tumour. The invention is also useful in gene therapy. The present sequence is human criptin growth factor (GGF) protein.

Sequence 223 AA;

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2000US - 0226681P

2000US - 0226681P

2000US - 0227182P

2000US - 0227182P

2000US - 0229287P

2000US - 0231243P

2000US - 0231248P

2000US - 0231248P

2000US - 0231248P

2000US - 0231289P

2000US - 0231289P

2000US - 023139P

2000US - 023143P

2000US - 023163P

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2000US - 024178P

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27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
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                                                                                                          MTWRHHVRLETVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE
                                                                                                                                                                                                VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR
                                                                 Gaps
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                             Length 223;
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                                                                                                                                                                                                                                                                                                                                                                                                 Novel human uterine motility-association polypeptide #29
                      Query Match
100.0%; Score 1249; DB 8;
Best Local Similarity 100.0%; Pred. No. 2e-95;
Matches 223; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU18122 standard; protein; 229
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2000US-0180628P.
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2000US-0189174P.
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2000US-0199174P.
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2000US-0209467P.
2000US-0215135P.
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Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive;
            121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
                                                               LLPCALLHRLLRPDAPAHPRSLVPSVLQRERRPCGRPGLGHRL 223
                                                                                                                                                                                                            Human novel secreted protein, SEQ ID 269.
                                                                                                                                      AAU17028 standard; protein; 229
                                                                                                                                                                                                                                                                                                                                       preservative; antiproliferative
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2000US - 021647P
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2000US - 0217487P
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2000US-0225267P.
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23-AUG-2000;
30-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecules encoding 49 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
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08-DEC-2000; 2
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RR 18-NV-20009-03494P.

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Length 229;

Query Match
100.0%; Score 1249; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.1e-95;
Matches 223; Conservative 0; Mismatches 0;

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2000US-0227182P.
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ABB10300
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WO200155304-A2.
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14-A0G-2000;

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14-A0G-2000;

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14-A0G-2000;

18-A0G-2000;

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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                 Homo sapiens.
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                                                     06-DEC-2001
                                                                                       Novel human
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                     AAU19904;
     SECGALEHGAWTLRACHLCRCIFGALHCLPLOTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence is a protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; SEQ ID NO 608; 859pp + Sequence Listing; English
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17-NOV-2000; 2000US-0249212P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-025198P.
05-DEC-2000; 2000US-0251868P.
06-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
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05-JAN-2001; 2001US-0259678P.
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Best Local Similarity 100.
Matches 223; Conservative
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N-PSDB; ABA06522.
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AAU19904 standard; protein; 229

AAU19904 ID AAUI

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Human; calcium-binding protein; calcium flux; neurological disease; immune dysfunction; digestive disorder; neoplastic disease; blood disorder; infectious disease; gene therapy; immunosuppressive; antiarthritic; cytostatic; vasotropic; antibacterial; nootropic; virucide.
                                              calcium-binding protein #13
                                                                                                                                                                                                                                                                                                                                                                                                                        2000US - 0179065P

2000US - 0186628P

2000US - 0186350P

2000US - 0189174P

2000US - 0198174P

2000US - 0198174P

2000US - 0198174P

2000US - 025515P

2000US - 0217487P

2000US - 0217487P

2000US - 0217487P

2000US - 021843P

2000US - 021843P

2000US - 021848P

2000US - 021848P

2000US - 021848P

2000US - 021848P

2000US - 021849P

2000US - 0225268P

2000US - 0225268P

2000US - 0225214P

2000US - 0225268P

2000US - 0225247P

2000US - 0225247P

2000US - 0225247P

2000US - 0225279P

2000US - 0225247P

2000US - 0225279P

2000US - 02253147P

2000US - 02292817P

2000US - 0229313P

2000US - 0229313P

2000US - 0239131P
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2000US-0232081P.
2000US-0231968P.
(first entry)
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PR 14-58P-2000; 2000US-022339P.
PR 14-58P-2000; 2000US-022339P.
PR 14-58P-2000; 2000US-022349P.
PR 14-58P-2000; 2000US-0223401P.
PR 14-58P-2000; 2000US-0223401P.
PR 14-58P-2000; 2000US-0223401P.
PR 14-58P-2000; 2000US-0233064P.
PR 25-58P-2000; 2000US-023493P.
PR 25-67CT-2000; 2000US-023499P.
PR 25-67CT-2000; 2000US-024647P.
PR 25-67CT-2000; 2000US-0246252P.
PR 25-67CT-2000;
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The present invention relates to the isolation of novel human calciumbinding proteins, and cDNA (AAS31577-AAS31654) and genomic sequences binding proteins, and cDNA (AAS31577-AAS31654) and genomic sequences canceding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. amylotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe combined immunodeficiency, SLD), disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or infectious disease (e.g. acquired immunodeficiency syndrome, ALDS). The novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit activities mediated by calcium-binding proteins. The polynucleotides of the invention are also useful in gene therapy. AAD19982-AAD19989 reperseent the novel human calcium-binding proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding a calcium-binding protein is used in preventing, treating or ameliorating a medical condition.
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                                                                                                                                                                                                                                                                    Ruben SM
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            05-DEC-2000; 2000US-0251908P.
05-DEC-2000; 2000US-025619P.
06-DEC-2000; 2000US-025619P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-025199P.
08-DEC-2000; 2000US-025199P.
11-DEC-2000; 2000US-025199P.
                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                  Rosen CA, Barash SC,
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N-PSDB; AAS31589.
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Immunostimulant; antirheumatic; antiarthritic; neuroprotective; antidiabetic; antidatheric; antidiabetic; antidiabetic; antidatheric; antidiabetic; antidiabetic; antidiabetic; antidiament; thrombolytic; antiatherosclerotic; cytostatic; nephrotropic; antiparkinsonian; gynecological; virucide; antibacterial; antiarrhythmic; fungicide; HCFATO5; HWAAB95; HTNBMO1; immunodeficiency; autoimmune disorder; allergic reaction; cardiovascular; inflammatory condition; graft-versus-host disease; reproductive system; blood-related disorder; hyperproliferative; endocrine; neurological; respiratory; renal; infectious disease; gastrointestinal; gene therapy; heuroral growth; neuronal disorder; neuro-degenerative condition;
Novel human protein SEQ ID No 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0225268P.
2000US-0225270P.
2000US-0225447P.
2000US-0225757P.
2000US-0225757P.
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2000US-0229345P

2000US-0229539

2000US-0239513P

2000US-0234223P

2000US-0234223P

2000US-023423P

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2000US-023423P
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2000US 0218290P
2000US 022063P
2000US 022451BP
2000US 022451BP
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2000US-0228924P.
2000US-0229287P.
2000US-0229343P.
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2000US-0237037P.
2000US-0237038P.
2000US-0237038P.
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2000US-0236367P.
2000US-0236368P.
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2000US-0217487P.
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2000US-0214886P
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2000US-0251869P
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22-AUG-2000;
22-AUG-2000;
30-AUG-2000;
30-AUG-2000;
30-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
07-SEP-2000;
07-SE
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02-0CT-2000; 2
02-0CT-2000; 3
02-0CT-2000; 3
13-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
10-0CT-2000; 2
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29-SEP-2000;
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28-JUN-2000;
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The invention relates to an isolated polypeptide comprising a sequence at least 90% identical to a full length protein sequence selected from 55 sequences given in the specification such as a sequence of 163, 74 or 140 amino acids fully defined in the specification, or the encoding sequence contained in 49 cDNA clones given in specification, or the encoding sequence of THNBMOL. The protein and its encoding nucleic acid are useful for diagnosing a pathological condition or susceptibility to a pathological condition in a subject and for preventing, treating or ameliorating a medical condition. The protein, its encoding nucleic acid and an isolated antibody that can bind to the protein are useful in treating, preventing, diagnosing and/or prognosing immunodeficiencies, autoimmune disorders, allergic reactions and conditions, inflammatory conditions, graft-versushost disease, blood-related disorders, hyperproliferative disorders,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDORR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
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                                                                                                                                                                          Novel polypeptide useful for diagnosis, prognosis, prevention, and treatment of immune, hyperproliferative, renal, respiratory, cardiovascular, reproductive, endocrine, gastrointestinal and
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100.0%; Pred. No. 2.1e-95;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                     Disclosure; Page 268-269; 335pp; English.
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                                                                                        Barash SC;
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Best Local Similarity 100.
Matches 223; Conservative
                                                                                                                                                                                                                                                  neurological disorders.
                                                                                      Rosen CA, Ruben SM,
                                                                                                                                     WPI; 2002-665432/71
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; imunosouppressive; antibacterrial; vulnerary; antipacterrial; vulnerary; antipacterrial; vulnerary; antiparepressive; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabelic; antiulcer; anticonvulsant; antifungal; antiparastic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-2000; 2000US-0229345P.
05-SEP-2000; 2000US-0229509P.
06-SEP-2000; 2000US-0229513P.
21-SEP-2000; 2000US-0231413P.
21-SEP-2000; 2000US-0231427P.
25-SEP-2000; 2000US-023482P.
25-SEP-2000; 2000US-0235834P.
25-SEP-2000; 2000US-0235834P.
29-SEP-2000; 2000US-0235834P.
29-SEP-2000; 2000US-0235834P.
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02-0CT-2000; 2000US-0237037P.

02-0CT-2000; 2000US-0237039P.

02-0CT-2000; 2000US-0237039P.

13-0CT-2000; 2000US-0239935P.

20-0CT-2000; 2000US-024905P.

20-0CT-2000; 2000US-024960P.

20-0CT-2000; 2000US-0241809P.

10-NOV-2000; 2000US-0244617P.

17-NOV-2000; 2000US-0244617P.

17-NOV-2000; 2000US-0249617P.
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2000US-0224518F

2000US-022526F

2000US-0225270F

2000US-022547P

2000US-0225778F

2000US-022578F

2000US-022578F

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2000US-0229348F

2000US-0229348F

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2000US-0229348F
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2000US-0236370P.
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                                                                                                                                                                             17-JAN-2001; 2001US-00764853
                                                                                                                              US2002090672-A1.
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
22-AUG-2000;
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29-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-2000;
                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                    14-AUG-2000;
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The invention relates to novel genes (ABV83682-ABV84101) and proteins

(ABP66710-ABP67129) useful for preventing, treating or ameliorating

cmedical conditions e.g. by protein or gene therapy. The genes are

isolated from a range of human tissues disclosed in the specification.

CT he nucleic acids, proteins, antibodies and (ant) agonists are useful in

the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and

covarian cancer and other cancers of the adrenal gland, bone, bone marrow,

breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune

disorders e.g. Addison's disease, allergies, autoimmune haemolytic

anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,

multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)

cardiovascular disorders such as myocardial ischaemias; (d) wound healing

cardiovascular diseases e.g. cerebral anoxia and epilepsy; and (f)

cinfections diseases such as wiral, bacterial, fungal and parasitic

infections. Note: The sequence data for this patent did not form part of

the printed specification, but was obtained in electronic format directly

from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide, opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; carthritis; hyperproliferative disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
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                                                                                     Novel polypeptide useful for diagnosis, prognosis, prevention, and treatment of immune, hyperproliferative, renal, respiratory, cardiovascular, reproductive, endocrine, gastrointestinal and neurological disorders.
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Pred. No. 2.1e-95;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 1249;
Best Local Similarity 100.0%; Pred. No. 2.1
Matches 223; Conservative 0; Mismatches
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                 WPI; 2002-681727/73.
N-PSDB; ABV83859.
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Homo sapiens

Barash SC;

Ruben SM,

Rosen CA,

BARA/) ROSE/) (RUBE/)

ROSEN C A. RUBEN S M. BARASH S C.

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2000US - 0235836P.
2000US - 023637P.
2000US - 023637P.
2000US - 023637P.
2000US - 0236369.
2000US - 02363709.
2000US - 02363703P.
2000US - 0237037P.
2000US - 0237037P.
2000US - 0237037P.
2000US - 0237039P.
2000US - 024128P.
2000US - 0241809P.
2000US - 0241809P.
2000US - 0246417P.
2000US - 0246611P.
2000US - 0246611P.
2000US - 0246611P.
2000US - 0246611P.
2000US - 024621P.
2000US - 024621P.
2000US - 024621P.
2000US - 024621P.
2000US - 024921P.
2000US - 025931P.
2000US - 025919P.
2000US - 025919P.
2000US - 025919P.
2000US - 0251869P.
2000US - 0251869P.
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 29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
20-CCT-2000;
20-CC
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       2000US-0139065P.
2000US-0186628P.
2000US-0186628P.
2000US-018630P.
2000US-0189374P.
2000US-0199076P.
2000US-0199076P.
2000US-02094617P.
2000US-02094617P.
2000US-0211487P.
2000US-0211487P.
2000US-0211487P.
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2000US-0211487P.
2000US-022934P.
2000US-023939P.
2000US-02393P.
2000US-02394P.
2000US-02394P.
                                                                                                2001WO-US001320
                         WO200155441-A2
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24 - FEB - 2000)
26 - MAR - 2000)
27 - MAR - 2000)
28 - MAR - 2000)
29 - MAR - 2000)
21 - JAN - 2000)
29 - JUN - 2000)
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WO200190304-A2
 Homo sapiens.
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Matches
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                                                                                                                                                                                             The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to encoded secreted proteins. The nucleic acids and proteins are used to consider the reat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic municossays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune conspissmes of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiovascular disorders e.g. corneal infection, can many other disorders e.g. Alzheimer's disorders e.g. corneal infection, and many other disorders e.g. charges e.g. corneal infection, can also be used to aid wound healing and epithelial cell proliferation, to preserve the sin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present construction or sequence represents a novel secreted protein of the invention. Note: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
                                                             Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, hemophilia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR
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Pred. No. 8e-95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                  Claim 11; SEQ ID NO 198; 601pp; English
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Matches 222; Conservative
Barash SC,
                               WPI; 2001-476222/51
N-PSDB; AAS26862.
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Rosen CA,
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB890444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Cronn's disease, conditis, (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing conflows diseases such as myocardial ischaemias; (d) wound healing infections. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; SEQ ID NO 2712; 2081pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 99.4%; Score 1241; DB 5; Local Similarity 99.6%; Pred. No. 9.3e-95; es 222; Conservative 0; Mismatches 1;
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                                                                                                                                             19-MAY-2000; 2000US-0205515P.
                                                                      18-MAY-2001; 2001WO-US016450
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                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                  Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-122018/16.
                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABL90745
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29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders.
                                                                                                                                                                                                                                                                                                  Birse CE,
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Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
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                                                                                                                                                                                                                                                                                                                                                                                             Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                  Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:422
                                                    181 LLPCALLHRLLRPDAPAHPRSLVPSVLQRERRPCGRPGLGHRL
                                                                              181 LLPCALLHRILRPDAPAHPRSLVPSVLQRERRPCGRPGLGHRL
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Wilson KE,
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                                                                                                                                                                                                                 ADN39104 standard; protein; 223 AA
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R, Watson SR,
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2001US-0334393P.
2001US-0335394P.
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08-JAN-2002; 2002US-0347211P.
10-JAN-2002; 2002US-0347349P.
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2002US-0372246P.
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                                                                                                                                                                                                                                                                                                            (first entry)
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N-PSDB; ADN39103.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003042661-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JAN-2002;
08-FEB-2002;
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DH,
                                                                                                                                                                                                                                                                 ADN39104;
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                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits to a sequence that is at least 80 % identical to a gene that exhibits in cased or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated polypeptide, for cancer in a patient and for treating a mammal lung cancer, nor-small cell for treating a modulatory compound identified. The methods are useful for treating a modulatory compound identified. The methods are useful corrector to other benign or precancerous lessions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary disease, fibrosis, bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic. compounds that modulate lung cancer, such as antibodies. Sequences and salvance to a salvance of the ABUS6745 represent lung cancer-susociated polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
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                                                         Lung cancer-associated polypeptide; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE
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                                                      polypeptide; cytostatic; emphysema;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
              Lung cancer-associated polypeptide #304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27; Page 426; 453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 2001US-0284770P.
2001US-0290492P.
2001US-0339245P.
2001US-0350666P.
2001US-0334370P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression in lung cancer.
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Best Local Similarity 99.6
Matches 222; Conservative
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N-PSDB; ABX76440.
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09-NOV-2001; 2
13-NOV-2001; 2
29-NOV-2001; 2
12-APR-2002; 2
                                                                                                                                                                                                 Unidentified
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Glynne R, 3, Zlotnik

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16-JUN-2005
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nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosting, prognosting and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atteroselerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistains syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                       MTWRHHVRLLFTVSLALQ1INLGNSYQREKHNGGREEVTKVATQKHRQSPLNWTSSHFGE
                                                                                                                                                                                                                                                                                                                                                                              MTWRHHVRLLFTVSLALQI INLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE
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                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                      Length 223;
                                                                                                                                                                                                                                                                                                                                   1; Indels
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Pred. No. 9.3e-95;
0; Mismatches 1;
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21-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-0333394P.
14-DEC-2001; 2001US-0340397P.
08-JAN-2002; 2002US-0347349P.
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2002US-0356714P.
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2002US-0368809P.
                                                                                                                                                                                                                                                                                      99.4%;
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2002US-0372246P.
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                                                                                                                                                                                                                                                                                                           Local Similarity 99.6
nes 222; Conservative
                                                                                                                                                                                                                                              Sequence 223 AA;
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04-APR-2002;
12-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-FEB-2002;
20-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUN-2004
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                                                                                                                                                                                                                                                                                      Query Match
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ADN39975
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention also relates to expression vectors and host cells comprising a nucleic acid of the invention, antibodies which specifically bind a polypeptide of the invention; antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and mucleic acids. The nucleic acids, polypeptides and methods are useful for disgnosting, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, attended acrossis, inflammatory diseases, autoimmune diseases, retinal neovascularistaton syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                             Hevezi PA;
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.4%; Score 1241; DB 7; Length 223; 99.6%; Pred. No. 9.3e-95; ive . 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Criptic protein, a member of the EGF-CFC family Seq 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LLPCALLHRILRPDAPAHPRSLVPSVLORERRPCGRPGLGHRL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLPCALLHRLLRPDAPAHPRSLVPSVLQRERRPCGRPGLGHRL 223
                                                                                                                                                                                                                                                                                Glynne R,
3, Zlotnik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents a polypeptide of the invention.
                                                                                                                                                                                                                                                                             Gish KC, Gl
Wilson KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; SEQ ID NO C345; 1385pp; English.
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                                                                                                                                                                                                                                                                             Ginsburg WM,
2, Watson SR,
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05-JUN-2002; 2002US-0386614P.
16-JUL-2002; 2002US-0396839P.
22-JUL-2002; 2002US-0397775P.
22-JUL-2002; 2002US-0397845P.
                                                                                                                                                                                                               (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                          09-SEP-2002; 2002US-0409450P
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Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                     Murray R,
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-468649/44.
                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADN39758.
                                                                                                                                                                                                                                                                                    Aziz N,
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This invention relates to a novel method for augmenting signaling of a ligand of a receptor serine kinase within a cell by inhibiting the formplexes between Cripto and this ligand on the surface of the cell. Specifically, it refers to TGF-beta and activin which are the ligands of serine kinase receptors and which regulate tissue homeostasis by activating the Samad2/3 intracellular signaling pathway is associated with oncogenesis and tumorigenesis. As such, the present invention describes a method for augmenting Smad2/3 signaling pathway is associated with oncogenesis and tumorigenesis. As such, the present invention describes a method for augmenting Smad2/3 angualing in a cell by administering a mutant ligand that retains signaling activity but is unable to bind to Cripto, and thus bypasses antagonism by Cripto. Note that augmentation of signaling increases the proliferative rate of the cell. The receptor serine the decreases the proliferative rate of the cell. The receptor serine kinase is a type I activin receptor-like kinases of of factor and the formation of complexes is inhibited by suppressing expression of cripto using antisense oligonucleocides (siRNA) directed against Cripto, and also mutating at least one allele of Cripto by homologous recombination. Accordingly, pharmaceutical compositions derived thereof exhibit cytostatic activity. This polypeptide sequence is the human Criptic procein, amember of the EGF-CFC (Epidermal Growth Factor-Cripto).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
                                                                                                                                                                                                                                                                                                                                                                          Augmenting signaling of a ligand of receptor serine kinase in a cell comprises inhibiting the formation of complexes between Cripto and the ligand on the surface of the cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGREEVTKVATQKHRQSPLNWTSSHFGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 4; 60pp; English.
                                                                                                                                                                                                                                                                                           Harrison CA;
                                                                                                                                                       14-SEP-2004; 2004WO-US029967
                                                                                                                                                                                                15-SEP-2003; 2003US-0503046P
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Matches 222, Conservative
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                                                                                                                                                                                                                                                                                           Gray PC,
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                                                                 WO2005028433-A2
                       Homo sapiens
                                                                                                             31-MAR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents the novel human cryptic-like secreted protein of the invention. The polypeptide of the invention has cytostatic, cardiant, nocropic, neuroleptic, antiasthmatic, and anti-angiogenic activity, and has a use in gene therapy. The polypeptide and polynucleotide of the invention may be used to treat cancer, particularly lung cancer, respiratory diseases, asthma, epilepsy, schizophrenia, depression, hyperactivity, heart hypertrophy, heart failure, cardiomyopathies, aberrant angiogenesis and vasculogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                     Cryptic; human; cytostatic; cardiant; nootropic; neuroleptic; cancer; antiasthmatic; anti-angiogenic; gene therapy; lung cancer; asthma; respiratory disease; epilepsy; schizophrenia; depression; hyperactivity; heart heart ailure; cardiomyopathy; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel cryptic-like secreted polypeptide found in various tumors and organs is useful to treat diseases including cancer, particularly lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTWRHHVRLLFTVSLALQIINLGNSYQREKHNGGRGEVTKVATQKHRQSPLNWTSSHFGE
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98.7%; Score 1233; DB 5;
Best Local Similarity 99.1%; Pred. No. 4.3e-94;
Matches 221; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 33-34; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer, asthma and heart disease
                                          Human cryptic-like polypeptide.
                                                                                                                                                                                                                                                                   36-APR-2001; 2001WO-EP003965
                                                                                                                                                                                                                                                                                                 10-APR-2000; 2000EP-00107142
           (first entry)
                                                                                                                                                                                                                                                                                                                               (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-017462/02.
                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH77168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 223 AA;
                                                                                                                                                                                                      WO200177322-A1
                                                                                                                                          vasculogenesis
                                                                                                                                                                        Homo sapiens.
              23-JAN-2002
                                                                                                                                                                                                                                    18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-APR-1997
                                                                                                                                                                                                                                                                                                                                                                Duecker K;
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AAG77914 standard; protein; 223 AA.

RESULT 14 AAG77914 AAG77914;

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SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human criptin growth factor (CGF) (AAW09111) is a novel polypeptide structurally related to human cripto growth factor. It is overexpressed and secreted by certain types of cancer cells, e.g. pancreatic cancers. Recombinant CGF can be produced in host cells utilising vectors incorporating a CGF cDNA clone (AATS1058) isolated from a human pancreatic cancer tissue cDNA library. CGF can be used to treat e.g. muscle wasting diseases, osteoporosis, to aid implant fixation, to stimulate tissue regeneration and wound healing, to promote angiogenesis and to stimulate proliferation of vascular smooth muscle and endothelial cell prodn. It can also be used as a marker for cancer diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human Criptin Growth Factor polypeptide - which can be used to stimulate angiogenesis and develop products for use in diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels 12; Gaps
                                                 Criptin growth factor; CGF; angiogenesis; wound healing; vulnerary; muscle wastage; osteoporosis; implant fixation; tissue regeneration; pancreas cancer; diagnosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 83.6%; Score 1044; DB 2; Length 230; Best Local Similarity 91.4%; Pred. No. 2e-78; Matches 191; Conservative 1; Mismatches 5; Indels 1;
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|LPCA-----TPAPASCARMRPRTLGP 202
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/label= Sig_peptide
                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                             95WO-US007087.
                                                                                                                                                                                                                                                                                                                                               95WO-US007087.
                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                 Human criptin growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                        Coleman TA;
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N-PSDB; AAT51058.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Meissner PS,
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                                                                                                                                                                                                                                                                                                                                               05-JUN-1995;
                                                                                                                             Homo sapiens
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NUMBER OF SEQUENCES: 7

Perfect score:

Title:

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Scoring table:

Word size :

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Query Match
Best Local Similarity 100.0%;
Matches 223; Conservative 0
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US-09-764-893-98
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198, App
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                                                                                                                                         (without alignments)
593.660 Million cell updates/sec
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                                                                                                                                                                                                                         223
1 MTWRHHVRLLFTVSLALQII......PSVLQRERRPCGRPGLGHRL 223
                                                                                                                  September 7, 2006, 12:35:51 ; Search time 174 Seconds
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Publication No. US20040086967A1
GENERAL INFORMATION:
APPLICANT: Meissner, Paul S.
COleman, Timothy A.
TITLE OF INVENTION: Human Criptin Growth Factor
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US-09-764-893-98
US-09-764-881-101
US-09-764-881-101
US-09-764-898-269
US-09-764-891-101
US-10-273-881-101
US-10-273-881-101
US-10-2742-101
US-10-25-027-422
US-10-264-227-21293
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US-10-257-113-2
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                                                                              OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Match Length DB
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Score

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61 VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR 120
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Publication No. US20020086330A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUCleic Acids, Proteins, and Antibodies

FILE REFERENCE: P2029

CURRENT APPLICATION NUMBER: US/09/764,893

CURRENT PILING DATE: 2001-019

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 154

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: 105/10/665,602

FILING DATE: 22-Sep-2003

CLASSIFICATION: Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/09/393,023A

FILING DATE: 09-SEP-1999

APPLICATION NUMBER: US 08/471,371

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:
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Pred. No. 1.4e-196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Marks, Michelle S.
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PF200D1
                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                        ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 301-309-6439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acida
TYPE: amino acid
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
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US-09-764-898-269
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                                                   FEATURE:
NAME/KEY: SITE
LOCATION: (2)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                  . LOCATION: (3)
. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-893-98
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PT207
CURRENT APPLICATION NUMBER: US/09/764,881
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 192
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 101
                                                                                                                                                                                                                            Query Match 100.0%; Score 223; DB 3; Length 229; Best Local Similarity 100.0%; Pred. No. 1.5e-196; Matches 223; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0
Matches 223; Conservative
                TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-764-881-101
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US-09-764-881-101
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LENGTH: 229
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FEATURE:
NAME/KEY: SITE
LOCATION: (2)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (3)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-608
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Fatent No. US20020090673A1
GENERAL INFORMATION:
FATELL OF INVENTION:
TILLE OF INVENTION:
FILE REFERENCE: DJZ01
CURRENT FILING DATE: 2001-01-17
Prior application date removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 311
SOFTWARE PATENTIN Ver. 2.0
SEQ ID NO 269
LENGTH: 229
                                                                                                                                                                                                                                                                Sequence 608, Application US/09764853
; Sequence 608, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE REFERENCE: PJZ06
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 608
: LENGTH: 229
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US-10-242-747-101
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE 1.00CATION: (3)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-898-269
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Publication No. US20030125246A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PT207
CURRENT APPLICATION NUMBER: US/09/764,881
CURRENT PELING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 101
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US-09-764-881-101
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

    NAME/KEY: misc_feature
    LOCATION: (3)
    OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-242-747-101

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APPLICANT: Afar, Daniel
APPLICANT: Gibberg, wendy M.
APPLICANT: Gibberg, wendy M.
APPLICANT: Gibh, Kurt C.
APPLICANT: Gibh, Kurt C.
APPLICANT: Howerl, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Wateon, Susan R.
APPLICANT: Wetson, Susan R.
APPLICANT: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Diagnosis of Cancer, TITLE OF INVENTION: Methods of Screening for Modulators of Cancer, CURRENT APPLICATION NUMBER: 103/10/295,027
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PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR PILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PATENTIN VET: 2.0
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PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/332,464
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Publication No. US20030232350A1
GENERAL INFORMATION:
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APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Ginaberg, Wendy M.
APPLICANT: Ginaberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Marson, Susan R.
APPLICANT: Warson, Susan R.
APPLICANT: Warson, Susan R.
APPLICANT: Warson R.
APPLICANT: Marson R.
APPLICANT: Marso
PRIOR APPLICATION NUMBER: US 60/340,376

PRIOR FILING DATE: 2001-12-14

PRIOR FILING DATE: 2001-12-14

PRIOR FILING DATE: 2002-01-08

PRIOR FILING DATE: 2002-01-08

PRIOR FILING DATE: 2002-01-08

PRIOR FILING DATE: 2002-01-10

PRIOR PRIOR APPLICATION NUMBER: US 60/355,250

PRIOR FILING DATE: 2002-02-08

PRIOR FILING DATE: 2002-02-13

PRIOR FILING DATE: 2002-02-13
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83.9%; Score 187; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.8e-163;
Matches 187; Conservative 0; Mismatches 0;
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; Publication No. US20030232350A1
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US-10-295-027-422
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157 CDPKDFLASHAHGPSAGGAPSLLLLPCALLHRILRPDAPAHPRSLVPSVLQRERRPCGR 216
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                                                                                                                                                                                                                                                                Sequence 4, Application US/10940431
; Sequence 4, Application US/10940431
; Publication No. US20050208045A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie
; APPLICANT: Harrison, Craig A.
; TITLE OF INVENTION: Cripto Antagonism of Activin and TGF-(; TITLE OF INVENTION: Signaling
; FILE REFERENCE: D6525
; CURRENT APPLICATION NUMBER: US/10/940,431
; CURRENT APPLICATION NUMBER: US/10/940,431
; CURRENT APPLICATION NUMBER: 60/503,046
; RIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Macintosh OS 10
; SEQ ID NO 4
; SEQ ID NO 4
; LENTH: 223
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 198
LENGTH: 231
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Sequence 198, Application US/09764898
Sequence 198, Application US/09764898
Sequence 198, Application US/09764898
SENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ01
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
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PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR PLUING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR PLUING DATE: 2002-01-10
PRIOR PLUING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: Petentin Ver. 2.1
SEQ ID NOS: 1238
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Matches 187; Conservative
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Best Local Similarity 100.
Matches 187; Conservative
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; ORGANISM: Homo sapiens
US-10-295-027-1293
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US-10-264-237-2712
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LENGTH: 223
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                                                                                                                                                                       45 EVTKVATQKHRQSPLNWTSSHFGEVTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGT 104
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                                                                       Query Match 83.9%; Score 187; DB 3; Length 231; Best Local Similarity 100.0%; Pred. No. 1.9e-163; Matches 187; Conservative 0; Mismatches 0; Indels
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65.0%; Score 145; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-125;
Matches 145; Conservative 0; Mismatches 0; Indels
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; Publication No. US20030207293A1
; Publication No. US20030207293A1
; GENERAL INFORMATION:
; APPLICANT: DUCKER, KLAUS
; TITLE OF INVENTION: CRYPTIC-LIKE SECRETED PROTEIN
; FILE REFERENCE: MERCK-2519
; CURRENT APPLICATION NUMBER: US/10/257,113
; CURRENT FILING DATE: 2001-04-06
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO SEQ ID NOS: 2
; SEQ ID NO SEQ ID NOS: 2
; SEQ ID NO SEQ ID NOS: 2
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Job time : 175 secs
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// ORGANISM: Homo sapiens

US-10-257-113-2
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OM protein - protein search, using sw model Run on:

7, 2006, 11:59:20; Search time 49 Seconds (without alignments) 398.354 Million cell updates/sec September

US-10-665-602-2 1249 Perfect score:

1 MTWRHHVRLLFTVSLALQII........PSVLQRERRPCGRPGLGHRL 223 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Issued\_Patents\_AA:\*
: / FWG Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*
: / FWG Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*
: / FWC Celerra\_SIDS3/ptodata/2/iaa/T\_COMB.pep:\*
: / FWC Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*
: / FWC Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*
: / FWC Celerra\_SIDS3/ptodata/2/iaa/RECOMB.pep:\*
: / FWC Celerra\_SIDS3/ptodata/2/iaa/RECOMB.pep:\*
: / FWC Celerra\_SIDS3/ptodata/2/iaa/RECOMB.pep:\*
: / FWC Celerra\_SIDS3/ptodata/2/iaa/RE

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 2, Appli	٦,	12.	7,	7,	7,	4,	4,	4	4,	4	ž.	'n	'n	'n	'n	7,	Seguence 8959, Ap	Sequence 11113, A	'n	'n	'n	Sequence 5, Appli	200	Patent No. 5256643	Sequence 14, Appl
ID	US-08-471-371-2	US-08-441-629-7	US-08-776-207-7	US-09-507-773-7	US-10-016-447-7	PCT-US95-09172-7	US-08-441-629-4	US-08-776-207-4	US-09-507-773-4	US-10-016-447-4	PCT-US95-09172-4	5256643-3	US-07-749-001-3	US-08-154-198-3	US-08-463-335-3	US-08-464-023A-3	US-08-471-371-7	US-09-949-016-8959	US-09-949-016-11113	US-07-749-001-5	US-08-154-198-5	US-08-463-335-5	US-08-464-023A-5	US-09-949-016-7062	5256643-2	US-08-208-008C-14
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Length	230	160	160	160	160	160	190	190	190	190	190	174	188	188	188	188	188	192	192	188	188	188	188	192	187	94
& Query Match	83.6	21.1	21.1	21.1	21.1	21.1	19.9	19.9	19.9	19.9	19.9	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.0	18.0	18.0	18.0	18.0	17.9	12.6
Score	1044	264	264	264	264	264	248.5	248.5	248.5	248.5	248.5	233	233	233	233	233	233	233	233	225	225	225	225	225	224	157
Result No.	-	7	٣	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26

Sequence 5, Appli Sequence 3, Appli Sequence 34, Appli Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appli Sequence 4, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 2, Appli
US-08-872-855-5 US-10-006-011A-4 US-08-820-170A-34 US-09-273-565-34 US-09-273-565-34 US-09-661-468-34 US-09-976-165-34 US-09-976-165-34 US-09-976-165-34 US-09-976-165-34 US-09-976-165-34 US-09-976-165-34 US-09-976-165-34 US-09-976-165-34 US-09-976-165-34 US-09-978-12-12 US-09-08-132-12 US-09-612-2268-2 US-09-612-2268-2 US-09-613-2268-2 US-09-113-825-2 US-09-113-825-2 US-09-113-825-2
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713 705 810 810 810 810 810 722 722 722 722 722 722 722 722 722 72
127.5 123 123 123 123 123 120.5 120.
7 7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

## ALIGNMENTS

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ADDRESSER CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, ADDRESSEE: STEWART & OLSTEIN STREET: 6 Becker Farm Road CITY: Roseland STATE: N.J.
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,371
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                         GENERAL INFORMATION:
APPLICANT: Meissner, Paul S.
APPLICANT: Coleman, Timothy A.
TITLE OF INVENTION: HUMAN CRIPTIN GROWTH FACTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32580-455
TELECOMMUNICATION:
TELEPHONE: (201) 994-1700
                                          ; Sequence 2, Application US/08471371
; Patent No. 5981215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (201) 994-1700
TELEFAX: (201) 994-1744
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 230 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                   STATE: N.J.
COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                             ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
RESULT 1
US-08-471-371-2
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83.6%; Score 1044; DB 1; Length 230; 91.4%; Pred. No. 2.6e-100; tive 1; Mismatches 5; Indels 12 Best Local Similarity 91.4 Matches 191, Conservative US-08-471-371-2 Query Match

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GENERAL INFORMATION:
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                                     61 VIGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGICVLGSFCVCPAHFIGRYCEHDQRR 120
                                                                                                                                                                                     SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRR 120
                                                                                                                                           121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
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43.5%; Pred. No. 1.7e-19;
tive 7; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08441629;
Patent No. 5766923;
GENERAL INFORMATION:
APPLICANT: Kinschner, Marc W.
APPLICANT: Kinschner, More 5766231yuki
TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
NUMBER OF SEQUENCES:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER EADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: DatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,629
FILING DATE: 15-MAY-1995
CLLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/279,217
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: HU95-01A
TELECOMMUNICATION INFORMATION:
TELECOMENICATION INFORMATION:
TELECOMENICATION OF SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 160 amino acids
TYPE: amino acids
TYPE: AND SEC SEQ IS SEC SEC SECONDER SECOND
                                                                                                                                                                                                                                                                                           181 LLPCALLHRLLRPDAPA-----HPRSLVP 204
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US-08-776-207-7
; Sequence 7, Application US/08776207A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Lexing.c..
STATE: Massachusetts
COUMTRY: USA
ZIP: 02173
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Matches 50; Conservative
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MOLECULE TYPE: protein
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US-08-441-629-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Indels 14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
21.1%; Score 264; DB 2;
Best Local Similarity 43.5%; Pred. No. 1.7e-19;
Matches 50; Conservative 7; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09507773
Sequence 7, Application US/09507773
Patent No. 6399386
GENERAL INFORMATION:
APPLICANT: Kirschner, Marc W.
APPLICANT: Kinschler, No. 6399386iyuki
TITLE OF INVENTION: Receptor-Ligand Assay
FILE REFERENCE: HU95-01A2
CURRENT APPLICATION NUMBER: US/09/507,773
CURRENT FILING DATE: 2000-02-18
PRIOR PILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/776,207
PRIOR APPLICATION NUMBER: 08/776,207
PRIOR APPLICATION NUMBER: 08/79,207
PRIOR APPLICATION NUMBER: 08/279,217
PRIOR APPLICATION NUMBER: 08/279,217
PRIOR FILING DATE: 1994-07-22
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 160
GENERAL INFOGRATION

APPLICANT: Kirschner, Marc W.
APPLICANT: Kinschies, No. 6080718iyuki
TITLE CO INVENTION: Receptor-Ligand Assay
FILE REFRENCE: HU95-01A2
CURRENT APPLICATION NUMBER: US/08/776,207A
CURRENT FILING DATE: 1995-07-19
EARLIER APPLICATION NUMBER: PC1/US95/09172
EARLIER APPLICATION NUMBER: PC1/US95/09172
EARLIER PILING DATE: 1995-05-15
EARLIER PILING DATE: 1995-05-15
EARLIER FILING DATE: 1994-07-22
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FRAESEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Mus musculus
US-08-776-207-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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--GEGASARPRCCRNGGTCVLGSFC 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 VCPAHFTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCD 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 ACPPSFYGRNCEHDVRKEHCGSILHGTWLPKKCSLCRCWHGQLHCLPQTFLPGCD 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 190;
                                                                                                                                                                                                                                                                                  Query Match 21.1%; Score 264; DB 5; Length 160; Best Local Similarity 43.5%; Pred. No. 1.7e-19; Matches 50; Conservative 7; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER TABLABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/441,629
FILING BATE: 15-MAY-1995
CLASSIFICATION 2435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/217
FILING BATE: 22-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 19.9%; Score 248.5; DB 1; Best Local Similarity 52.9%; Pred. No. 8.4e-18; Matches 37; Conservative 13; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                           58 FGEVTG-----SAEGWGPEEPLPYSRAF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Kirschner, Marc W.
APPLICANT: Kinoshita, No. 5766923iyuki
TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REPERENCE/DOCKET NUMBER: HU95-01A
TELECOMMUNICATION INFORMATION:
TELECPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08441629 Patent No. 5766923
                     TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Two Militia Drive
(617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                   LENGTH: 160 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                         single
                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Two Militia I
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                                                                                              TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02173
  TELEPHONE:
                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                     PCT-US95-09172-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-441-629-4
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                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            요
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                                        Sequence 7, Application US/10016447

Patent No. 6844193

GENERAL INFORMATION:
APPLICANT: Kirschner, Marc W.
APPLICANT: Kirschner, Marc W.
APPLICANT: Kinoshita, No. 6844193iyuki
APPLICANT: Kinoshita, No. 6844193iyuki
TITLE OF INVENTION: Receptor-Ligand Assay
FILE REFERENCE: HU95-01A2
CURRENT APPLICATION NUMBER: US/10/016,447
CURRENT APPLICATION NUMBER: EARLIER PILING DATE: 1997-06-23
FRIOR FILING DATE: EARLIER FILING DATE: 1997-06-23
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/441,629
FRIOR FILING DATE: EARLIER FILING DATE: 1995-05-15
FRIOR PAPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/279,217
MINDED OF SEC TO NO. 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 ACPPSFYGRNCEHDVRKEHCGSILHGTWLPKKCSLCRCWHGQLHCLPQTFLPGCD 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.1%; Score 264; DB 2; Length 160; 43.5%; Pred. No. 1.7e-19; ive 7; Mismatches 44; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kirschner, Marc W.
APPLICANT: Kinoshita, Noriyuki
TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: HU95-01A PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/41,629
FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application PC/TUS9509172 GENERAL INFORMATION:
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Best Local Similarity 43.5
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
ZIP: 02173
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89 RCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHC 148

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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/09172
  37; Conservative 13; Mismatches
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APPLICANT: Kinoshita, Noriyuki
TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
CORRESPONDENCE: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application PC/TUS9509172
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10016447 Patent No. 6844193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT; ORGANISM: Xenopus laevis
US-10-016-447-4
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142 FKPESED-CD 150
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                                                                                                                                   149 LPLQTPDRCD 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
PCT-US95-09172-4
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US-10-016-447-4
    Matches
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                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Kirschner, Marc W.
APPLICANT: Kirschner, Marc W.
APPLICANT: Kirschner, Mo. 6080718iyuki
ITLE OF INVENTION: Receptor-Ligand Assay
FILE REFERENCE: HU95-01A2
CURRENT APPLICATION NUMBER: US/08/776,207A
CURRENT FILING DATE: 1997-06-23
EARLIER PILING DATE: 1997-06-23
EARLIER FILING DATE: 1995-07-19
EARLIER PILING DATE: 1995-07-19
EARLIER PILING DATE: 1995-07-19
EARLIER PILING DATE: 1995-07-15
EARLIER PILING DATE: 1995-07-22
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTHAL 190
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APPLICANT: Kinoshita, No. 6399386iyuki
TITLE OF INVENTION: Receptor-Ligand Assay
FILE REFERENCE: HU95-01A2
CURRENT APPLICATION NUMBER: US/09/507,773
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: 08/776,207
PRIOR PELING DATE: 1997-06-23
PRIOR FILING DATE: 1995-05-15
PRIOR APPLICATION NUMBER: 08/279,217
PRIOR FILING DATE: 1994-07-22
NUMBER OF SEQ ID NOS: 18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                        ; Sequence 4, Application US/08776207A; Patent No. 6080718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09507773
Patent No. 6399386
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Xenopus laevis
US-08-776-207-4
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US-09-507-773-4
                                                                    149 LPLQTPDRCD 158
                                                                                                              142 FKPESEĎ-ĆĎ 150
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LENGTH: 190
TYPE: PRT
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US-09-507-773-4
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89 RCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHC 148
                                                                                          89 RCCRNGGTCVLGSFCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHC
Gaps
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Indels
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APPLICANT: Kirschner, Marc W.
APPLICANT: Kirschner, Marc W.
APPLICANT: Kinschner, Mo. 6844193iyuki
TITLE OF INVENTION: Receptor-Ligand Assay
FILE REFERENCE: HU95-01A2
CURRENT APPLICATION NUMBER: US/10/016,447
CURRENT FILING DATE: 2010.12-10
PRIOR PILING DATE: EARLIER APPLICATION NUMBER: US/()
PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-23
PRIOR FILING DATE: EARLIER FILING DATE: 1995-05-15
PRIOR FILING DATE: EARLIER FILING DATE: 1995-05-15
PRIOR FILING DATE: EARLIER FILING DATE: 1995-05-15
PRIOR FILING DATE: EARLIER FILING DATE: 1994-07-22
NUMBER OF SEQ ID NOS: 18
SOFTWARR: FASTERE FILING DATE: 1994-07-22
SOFTWARR: FASTERE FILING DATE: DATE: BALIER FILING DATE: 1994-07-22
NUMBER OF SEQ ID NOS: 18
SEQ ID NOS: 18
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   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 19.9%; Score 248.5; DB 2; Best Local Similarity 52.9%; Pred. No. 8.4e-18; Matches 37; Conservative 13; Mismatches 19;
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NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
                                                           ZIP: 20036
COMPUTER READABLE FORM:
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Washington
                                                         20036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Sar
STATE: Ca
COUNTRY:
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                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 WPQEEP-----AIRPRSSQRVPPMGIQHSKELNRTCCLNGGTCMLGSFCACPPS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; Indels 30; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 18.7%; Score 233; DB 7; Length 174; Best Local Similarity 39.1%; Pred. No. 3.1e-16; Matches 43; Conservative 7; Mismatches 30; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Indels
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US-07-749-001-3
; Sequence 3, Application US/07749001
; Sequence 3, Application US/07749001
; GENEMAL INCRATION:
; APPLICANT: Salomon, David S.
; APPLICANT: Persico, Maria G.
; TITLE OF INVENTION: A HUMAN CRIPTO-RELATED GENE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

CTREET: 1615 L Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.9%; Score 248.5; DB 5 52.9%; Pred. No. 8.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Persico, Maria G.;Salomon, David S.
TITLE OF INVENTION: HUMAN CRIPTO PROTEIN
NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
FILING DATE: 29-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Mismatches
                                                                                                                                     NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: HU95-01A PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 WGPEEPLPYSRAFGEGASARPR-----
                 APPLICATION NUMBER: 08/279,217
FILING DATE: 22-JUL-1994
PRIOR APPLICATION DATA.
APPLICATION NUMBER: 08/441,629
FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                       TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                             LENGTH: 190 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 52.9
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                    single
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 LPLQTPDRCD 158
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                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Patent No. 5256643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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5256643-3
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68 WGPEEPLPYSRAFGEGASARPR--------CCRNGGTCVLGSFCVCPAH 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 FIGRYCEHDORRSECGALEHGAWTLRACHLCRCIFGALHCLPLOTPDRCD 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.7%; Score 233; DB 1; Length 188; 39.1%; Pred. No. 3.4e-16; tive 7; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,198
FILING DATE: 17-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/749,001
FILING DATE: 23-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ...wiisend and Townsend Khourie and Crew II: Steuart Street Tower, One Market Plaza San Francisco : 'California 'Y: ne
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/749,001
FILING DATE: 19910823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08154198
Patent No. 5620866
GENERAL INFORMATION:
APPLICANT: SALOWON, David S.
APPLICANT: PERSICO, Maria G.
TITLE OF INVENTION: A HUMAN CRIPTO-RELATED GENE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               WTS/5683/91630/SRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                 FILING DATE: 19910823
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOLE, WALSON T.
REGISTRATION NUMBER: 26,581
REPRENCE/POCKET NUMBER: WTS/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
                                                                                                                                                                                                                                                                                                                                                                             TELEX: 248453 CUSH
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 188 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 39.1
Matches 43, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           ----CCRNGGTCVLGSFCVCPAH 108
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 FYGRNCEHDVRKENCGSVPHDTWLPKKCSLCKCWHGQLRCFPQAFLPGCD 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 FTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCD 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                          Query Match
18.7%; Score 233; DB 1; Length 188;
Best Local Similarity 39.1%; Pred. No. 3.4e-16;
Matches 43; Conservative 7; Mismatches 30; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 233; DB 1; Length 188;
Pred. No. 3.4e-16;
7; Mismatches 30; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CONTAME: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,335
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,001
FILING DATE: 32-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: SCOCT: WALSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/91630/SRL
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TELEPHONE: (202) 861-3000
TELEPHONE: (202) 862-0944
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CRARACTERISTICS:
LENGTH: 188 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08463335;
Sequence 3, Application US/08463335;
Batent No. 5650285;
APPLICANT: Salomon, David S. APPLICANT: Persico, Maria G. TITLE OF INVENTION: A HUMAN CRIPTO-RELATED GENE NUMBER OF SEQUENCES: 5;
CORRESPONDENCE ADDRESS: ADDRESSE: CUSHMAN, DARBY & CUSHMAN STREET: 1615 L Street, N.W. CITY: Washington STATE: D.C. CITY: Washington STATE: D.C. CUNTRY: USA
TELERONGINICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                  68 WGPEEPLPYSRAFGEGASARPR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.7%;
39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acids
TOPOLOGY: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 39.1
Matches 43; Conservative
                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-154-198-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-463-335-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-08-463-335-3
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